

GenCore version 4.5
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OM nucleic - nucleic search, using SW model

Run on: February 18, 2001, 19:19:51 ; Search time 3075.67 Seconds
(Without alignments)
6383.969 Million cell updates/sec

Title: US-09-143-828-3
Perfect score: 2802
Sequence: 1 tgaattcgctggcctgctg.....aaaaaaaaaaaaaaaaaaaaa 2802

Scoring table: IDENTITY_MNC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
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 187: em_estp86:*
 188: em_estp87:*
 189: em_estp88:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	523.2	18.7	638	AV651714	AV651714 AV651714
2	445.2	15.9	461	AA699679	AA699679 z178c07.s
3	416	14.8	454	N94132	N94132 za25906.r1
4	340	12.1	343	AI248626	AI248626 qb77b12.x
5	338.2	12.1	794	AI746915	AI746915 u109a10.y
6	335	12.0	365	N69311	N69311 za25906.s1
7	201	7.2	472	AA277370	AA277370 va81a12.r
8	199.6	7.1	493	AM871811	AM871811 da94c06.y
9	185.4	6.6	200	AA679591	AA679591 z149d12.s
10	166.4	5.9	463	AM511148	AM511148 bd22a05.x
11	165.4	5.9	215	AV108557	AV108557 AV108557
12	156.8	5.6	432	AM158294	AM158294 za39e07.x
13	154.4	5.5	601	AM107536	AM107536 u191a06.y
14	143.8	5.1	501	AI768052	AI768052 w146b06.x
15	140.8	5.0	1053	AM012320	AM012320 um07d07.y
16	132.8	4.7	540	BE573696	BE573696 601333441
17	132	4.7	463	AI049239	AI049239 uc85f08.y
18	118	4.2	724	AI046425	AI046425 uc85f04.x
19	108.4	3.9	468	AA396982	AA396982 mx86a06.r
20	102	3.6	463	AA107961	AA107961 mp04d08.r
21	101.2	3.6	506	AA679391	AA679391 z129a02.s
22	100.8	3.6	616	AI238397	AI238397 GH14435.5
23	99.2	3.5	732	AI393915	AI393915 AJ393915
24	99	3.5	370	AI024672	AI024672 cv60b04.x
25	97.6	3.5	507	AA264990	AA264990 LD08b66.5
26	97.6	3.5	690	BE266478	BE266478 601192748
27	97.6	3.5	1105	BE101116	BE101116 601302405
28	97.2	3.5	589	BE275249	BE275249 601122072
29	94	3.4	851	BE877201	BE877201 601485121
30	90.2	3.2	708	BE390042	BE390042 601285233
31	88.8	3.2	692	BE791424	BE791424 601582442
32	88.6	3.2	392	AM505439	AM505439 UI-HR-BNO
33	88.6	3.2	475	BE664197	BE664197 148439.MA
34	86.6	3.1	539	AI098643	AI098643 uc32f10.y
35	83.6	3.0	623	BE303050	BE303050 ba72h10.y
36	83.4	3.0	788	BE915476	BE915476 601664976
37	82.8	3.0	665	BE390515	BE390515 601284134
38	82.4	2.9	467	AA570939	AA570939 v185f05.r
39	81.8	2.9	959	BE903117	BE903117 601677193
40	81.4	2.9	564	AV609965	AV609965 AV609965
41	81.2	2.9	771	BE385638	BE385638 601278159
42	81	2.9	248	AA272757	AA272757 vb09h12.r
43	81	2.9	514	AA124058	AA124058 mo29c08.r
44	80.4	2.9	667	AM231123	AM231123 uo35g12.y
45	80	2.9	563	BE233303	BE233303 139430.MA

ALIGNMENTS

RESULT 1
 AV651714
 LOCUS
 DEFINITION AV651714 G1C Homo sapiens cDNA clone G1CSCG03 3', mRNA sequence.
 AV651714
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

Qy	2210	taagtaaaaaaacaaacaaagaaacaaacaaacatttgatcaaaaaggagaataatgaatg	2269
Db	401	TAGTTAAAAAACAACAGAAACACAAACATTGGATAAAGAG-AAATGATACTG	343
Qy	2270	acaaaagcaagcacaaagaaatttcctctgtgtgaatgcagctgtgtatgtgcagcaatg	2329
Db	342	ACAAAAGAGACAAAGAAATTTCCCTGTGTGGATGCTGAGCTGTATGGCGGCACTGG	283
Qy	2330	taaccaagtgaaggttcctccgaagacatgatctgtctgtgagcaagggcccaaacatgcagct	2389
Db	282	TACCAAGTGAAGTTTCCCGAGACATGATCTGTGTGGAGCAAGGGCAACAACTGCACCT	223
Qy	2390	gtgaatgcgtgtgtgtgaatttggltgaaggaagtcgtgttcgaactatgtgggcctgg	2449
Db	222	GTGATGCGCTGTGTGTATTGTGGTGTAGGTAGTCTGTTGGCATTGATGGGGCTGGG	163
Qy	2450	ttgttcctgtggagctgtgaatcctgtgtatgctctgtgaacaagctacgctgaacaatcagt	2509
Db	162	TTTGTCTCTGGCGCTGGAAATGCTGGGATGCTGTGTGACAAACGTACGCTGCACATCAGT	103
Qy	2510	taaacacacggagaaagaacacatttaacatgcacacctatattctctgttaacaatctatc	2569
Db	102	TAAACACACCGGAAMAACATTATTACATCACTTATTTCTGTGTACACATCTATTTC	43
Qy	2570	tcaagctaaagggtatgaagatgcctgcctgtttatatgcc	2611
Db	42	TCAAGCTAAAGGTTATGAAGTCCCTGCCTTGTATTATGCC	1

RESULT	3				
NCBI32					
LOCUS					
DEFINITION	N94132	454 bp	MRNA	EST	05-APR-1996
ACCESSION	24259606.r1	Soares fetal liver spleen	INRLS	Homo sapiens	cdna clone
VERSION	N94132	IMAGE:293626.5,	mrna	sequence.	
KEYWORDS	N94132.1	GI:1266441			
SOURCE	EST.				
ORGANISM	human.				
REFERENCE	Homo sapiens				
AUTHORS	Euhayrout, Metzoca; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
TITLE	1 (bases 1 to 454)				
JOURNAL	Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.				
COMMENT	The WashU-Merck EST Project				
	Unpublished (1995)				
	Contact: Wilson RK				
	Washington University School of Medicine				
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
	Tel.: 314 286 1800				
	Fax: 314 286 1810				
	Email: est@wustl.edu				
	This clone is available royalty-free through INRL; contact the				
	IMAGE Consortium (info@image.lnl.gov) for further information.				
	Seq primer: mob.RBGA+ET				
	High quality sequence stop: 416.				

FEATURES

source

```

/organism="Homo sapiens"
/db_xref="GDB:3801473"
/db_xref="taxon:9606"
/clone_image="293626"
/clone_lib="Soares fetal liver spleen mNLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10 (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pUT73D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I oligo(dn) primer
15' AATCGGAGAGATTAAATTAAGACCTTTTTTTTTTTTTTTTTTT 3'}
```

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalisation. Library constructed by Bento Soares and M.Fátima Bonaldo."

Query Match	14.8%	Score 416	DB 143	Length 454
Best Local Similarity	98.4%	Pred. No. 7.4e-86		
Matches 441	Conservative	0	Mismatches 5	Indels 2
				Caps
QY 1802	agatcccaactaaagtgtcacaagctgtggaagggaaccaagagaccaaaggtatagccatctcg	1861		
DB 7	AGATCCCACTAAATGTCAAGGTGTGAAGGGACCAAGACCAAGATGGGCATCTGG	66		
QY 1862	ggctatagcccaactaccacacgtttgtcgcttcctcgagtcctttcattgtaacctaa	1921		
DB 67	GGCTATAGCCCACTACCCACGTTGTGTGGCTTCCGAGATCTTTTCATTGCTACTCTAA	126		
QY 1922	tagctctgctcccaacttcccaactgcttcacctcctcttcctcgagctgtttgtggctca	1981		
DB 127	TAGCTCTGTCTCCACTTCCCACTCGATCCCTCTCTCCAGATGCTTTGTGGGCTCC	186		
QY 1982	aggcctgtacccatcggcgaagtgcatagtatctctgtggagctccctctgagaagatggaa	2041		
DB 187	AGGCTGTACACCAACGGCAGCGCCATGAGATCTGTGGAGTCTCTAGAGATGACAA	246		
QY 2042	gccaggaagccctgacacaaatgtcagaagcttgacataccctcattcggccacatcat	2101		
DB 247	TCCAGAGAGCTGCACCAATGTCAAGCTTGGCATGACCTCATTCGGGCAACTATT	306		
QY 2102	ctgtgctctctgcacatcatcttgaaacacattattaagcaactgataataggtagctgtctg	2161		
DB 307	CTGTGCTCTCTCATCCATTGGAACAATATTATAGCACCGAATAAAGTAGCTGCTGTG	366		
QY 2162	gggtataagacatt-gagctagaatagatctcgg-gagtcacaagagttataagttaaaaa	2219		
DB 367	GGGTATAGAGATTGGACTAGATATATGATCCCTGAAGCTCTACAGAGTTATATGTTAAAA	426		
QY 2220	aacaaacgaaacacaacaaatttgat 2247			
DB 427	AACAAACGAAACAAACAATTTGGAT 454			

RESULT	4
AT248626/c	
LOCUS	AT248626 343 bp mRNA EST 01-DEC-1998
DEFINITION	qh7hb12.x1 Soares fetal_liver.spleen.INTLS.S1 Homo sapiens CDNA clone IMAGE1850687.3 similar to gb:J03258 VITAMIN D3 RECEPTOR (HUMAN); mRNA sequence.
ACCESSION	AT248626
VERSION	AT248626.1 GI:3844023

ORGANISM	Homo sapiens; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 343)
REFERENCE	NCI-CGAP. http://www.ncbi.nlm.nih.gov/ncicgap .
AUTHORS	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE	Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D.

This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert length: 608 Std Error: 0.00
 Seq primer: -40UP from G4bco
 High quality/sequence stop: 338.
 Location/Qualifiers

FEATURES

Query Match 7.28; Score 201; DB 4; Length 472;
 Best Local Similarity 77.2%; Pred. No. 4; 7e-36;
 Matches 294; Conservative 0; Mismatches 82; Indels 5; Gaps 4;

OY 1210 ccaatccctctctctccacagacgagcagtgctgcagacac-gcgcgtggtgagacag 1268
 |||||
 DB 1 CCAATCTCCCTCTTCTCCCAATGCTCTGCTGTCACAGCAGCTNNGTAGACCAA 60

OY 1269 ctgcagagagcaatctgcacatctacatgagcctacatctgacatcgccagcct 1328
 |||||
 DB 61 CTGACAGAGAGGTGTGGCTCACCCTGAAGGCTACATGAGTGTATCGGCAATACCT 120

OY 1329 gctcagaggtctctctctcctgaagatcagtgctacacagcagcgcagcagc 1388
 |||||
 DB 121 GCTCAGAGGTCTCTCTCTCTGAGATCATGAGCTCTCTCTCTCTCTCTCTCTCT 178

OY 1389 gctcagacacacacagcagcagcagcagcagcagcagcagcagcagcagc 1448
 |||||
 DB 179 GCCCAGCAACCCAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 238

OY 1449 atgcagagaggtctgcagcagcagcagcagcagcagcagcagcagcagcagc 1508
 |||||
 DB 239 ATGCAAGATTTATTAGACAGACAGATGCTGAGTGTGCTGCTGCTGCTGCTGCTG 298

OY 1509 gaggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1568
 |||||
 DB 299 GGGGAGCTAGACCCAGA-CATCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 356

OY 1569 gccaaagcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1589
 |||||
 DB 357 ACTGATACCCCAACACGCCCT 377

RESULT 8
 AM871811 493 bp mRNA EST 22-JUN-2000
 LOCUS da94c06.y1 Xenopus laevis tadpole stage 24 Xenopus laevis cDNA

DEFINITION clone IMAGE: 5' similar to gb:J03258 VITAMIN D3 RECEPTOR (HUMAN);
 mRNA sequence.

ACCESSION AM871811 GI:8005864
 VERSION AM871811.1 GI:8005864
 KEYWORDS EST.

SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 Xenopodidae; Xenopus.

REFERENCE 1 (bases 1 to 493)
 Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Page,D.,
 Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
 B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
 Waterston,R. and Wilson,R.
 Washu Xenopus EST project, 1999

TITLE Unpublished (1999)
 JOURNAL Other ESTs: da94c06.x1
 COMMENT Contact: Sandy Clifton, Ph.D.
 Washu Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Library constructed by B. Korn PhD. and S. Henze DNA Sequencing by:
 Washington University Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the Resource Center at the University of Maryland, Berlin, Germany (web
 address: www.rzpd.de)
 Seq primer: -40RP from GIDCO
 High quality sequence stop: 418.

FEATURES
 Source 1..493
 Location/Qualifiers
 1..493
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"

/clone="IMAGE:"
 /clone_lib="Xenopus laevis tadpole stage 24"
 /sex="mixed"
 /tissue_type="whole tadpole"
 /dev_stage="stage 24"
 /lab_host="DH10B"
 /note="Vector: pCMVSPORT6; Site_1: NotI; Site_2: SalI.
 Method of cloning used: directed ligation; InsertCheck:
 95.8 blue and 4.2 white. Library constructed by Dr.
 Bernhard Korn and Sabine Henze. Note: This is a Xenopus
 Gene Collection (XGC) library."
 BASE COUNT 129 a 142 c 131 g 91 t

Query Match 7.1%; Score 199.6; DB 96; Length 493;
 Best Local Similarity 68.1%; Pred. No. 1e-35;
 Matches 293; Conservative 0; Mismatches 134; Indels 3; Gaps 1;

OY 267 gcagatgagagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 326
 |||||
 DB 10 GAAGACAGACAGATGGGACCCCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 69

OY 327 tctcactcaatgctcagcagcagcagcagcagcagcagcagcagcagcagcagcag 386
 |||||
 DB 70 TATCACTTCAATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 129

OY 387 cgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 446
 |||||
 DB 130 AGGAACTTGGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAG 186

OY 447 cggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 506
 |||||
 DB 187 CGGCGCCACTGCGACAGCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 246

OY 507 atgatacttcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 566
 |||||
 DB 247 TTGATATGCTCCGATGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 306

OY 567 gaacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 626
 |||||
 DB 307 TTACAGAAATTCGCCCCACACTCCAGGCGCCAGCTGATCAGCAGCAGCAGCAGCAG 366

OY 627 atcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 686
 |||||
 DB 367 CTCACCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426

OY 687 aattccgcgc-696
 |||||
 DB 427 AACCTTCGGC-436

RESULT 9
 AA679591 200 bp mRNA EST 19-DEC-1997
 LOCUS zj49d12.s1 Soares fetal_liver_spleen_infls_s1 Homo sapiens cDNA

DEFINITION clone IMAGE:453623 3' similar to TR:6410518 G410518 ORPHAN NUCLEAR
 RECEPTOR OF STEROID/THYROID SUPERFAMILY. ; mRNA sequence.

ACCESSION AA679591 GI:2660113
 VERSION AA679591.1 GI:2660113
 KEYWORDS EST.

SOURCE Homo sapiens
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 200)
 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Getseil,G., Jost,S.,
 Kitzman,D., Kucada,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
 J., Moore,B., Scheinberg,K., Stepien,M., Tan,F., Theising,B.,
 White,Y., Wylie,T., Waterston,R. and Wilson,R.
 Washu-NCI human EST Project

TITLE Unpublished (1997)
 JOURNAL Contact: Wilson RK

JOURNAL
COMMENT

Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-reserch.riken.go.jp

Thermolabile and thermostable DNA polymerases by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (<http://genome.riken.go.jp>) for
further details.

FEATURES
source

Location/Qualifiers
1. 215
/organism="Mus musculus"
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Matches 184; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 340 tcatgacatgtgaagatgcaagagcttttcagagagggccatgaagcgaacccggc 399
DB 1 TCGAGACCGCTGAGATGAGAGGCTTTTTCAGCAGGCCCTGACACACATGTCGGC 60
QY 400 tggagtgcccttcggaagggcgctcgagatcaacccggaagcccgagcagtgcc 459
DB 61 TGAGCTGCGCTTTCGAGAGGAACTGCGAGATCACCCGAGAGACGAGCGGCACTGCC 120
QY 460 aggcctgcgcgcctgcgaagtgcttgagagggcgcatgaagagggatgcatgtccg 519
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QY 520 acgagggcctgtgagagagggcgcttgatcaag 554
DB 181 ATCGCGCTGTGAGAGAGCGGCGCTTGTATCAAG 215

RESULT 12
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LOCUS 2a39e07.x1 Xenopus EST library Xenopus laevis cDNA clone 2a39e07
DEFINITION 5' mRNA sequence.
ACCESSION AM158294.1 GI:6270323
VERSION EST.
KEYWORDS African clawed frog.
SOURCE Xenopus laevis
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE 1 (bases 1 to 432)
Schutz, K., de la Basile, M., Huang, E.-N., Nasclmento, L., Preston, R.,
Shah, R., Swaby, I., Shekher, M., Spiegel, L., Vill, M.D. and McComble
M.R.

TITLE Expressed sequence tags from Xenopus
JOURNAL Unpublished (1999)
CONTACT: W. Richard McComble
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884
Fax: 516 367 8874
Email: mcomble@csb.csh.riken.go.jp
Plate: 2a39 row: e column: 07
Seq primer: M13 universal forward primer
High quality sequence stop: 432.
Location/Qualifiers
1. 432

FEATURES
source

/organism="Xenopus laevis"
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/dev_stage="tadpole"
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was supplied by Holly Cline (Cold Spring Harbor Labs).
cDNA synthesis with Oligo dt Xba I (Xba I cloning site).
RNA: stage 50-56 tadpoles, total brain tissue, gtc
extraction method."

BASE COUNT 112 a 90 c 142 g 88 t
ORIGIN

Query Match 5.6%; Score 156.8; DB 40; Length 432;
Best Local Similarity 74.0%; Pred. No. 7.9e-26;
Matches 213; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 267 gcaatgaggaagtcggaagtcgcccaatctgcggtatgtgggacaagccatgyc 326
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QY 327 tctacatcaatgtcatcatcatgtgaagatgaagggcttttcagagagggccatgaa 386
DB 207 TATCATCTAATGCTATGACCTCGAGGCGCTGCAAGGATTTCTTACGCGGCGGTAG 266
QY 387 cgcacagccgcgctgaggtgccttcggaagggcgctgcgagatcaacccggaagacc 446
DB 267 AGGAATCTGCGGCTGAGGCTGCGCTTTCAGAA---TTCTCTGCTGATCAGACAGCAAT 323
QY 447 cggcagcagtcgcaagtcgctgcgccttcgcaagtgctggaagcggcagatgaagagag 506
DB 324 CGGCGCCACTCTCGAGGCTGCTGCTCAAGAAATGCTGACATCGGCAATGAGAAAGAG 383
QY 507 atgatacatgtccgagagggcgctgtgagagggcgcccttgatcaag 554
DB 384 TTGATCATGTCTGATGAGCGGCTGGAACAGAGAGAGCGGCTTAATTAG 431

RESULT 13
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LOCUS U191a06.x1 Suga mouse kidney m1a Mus musculus cDNA clone
DEFINITION IMAGE:2159410 5' similar to gb:00358 VIRAMIN D3 RECEPTOR (HUMAN);
gb:U15548 Mus musculus beta 2 thyroid hormone receptor (MUSE);
mRNA sequence.
ACCESSION AM107536
VERSION AM107536.1 GI:6078336
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 601)
Marr, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.

TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
CONTACT: U191a06.x1
Other ESTs: U191a06.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999

OY 588 ctgagagtcagagggctgacagagagcgatgatacagggagctgacgacgt 647
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 DB 34 CGCCATAGACCTATAGCGCGCTCCT 7

RESULT 15

BE573696 1053 bp mRNA EST 15-AUG-2000
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 mRNA sequence.
 ACCESSION BE573696
 VERSION BE573696.1 GI:9817416
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 TITLE 1 (bases 1 to 1053)
 JOURNAL NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.
 COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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 High quality sequence stop: 685.
 Location/Qualifiers

FEATURES

source

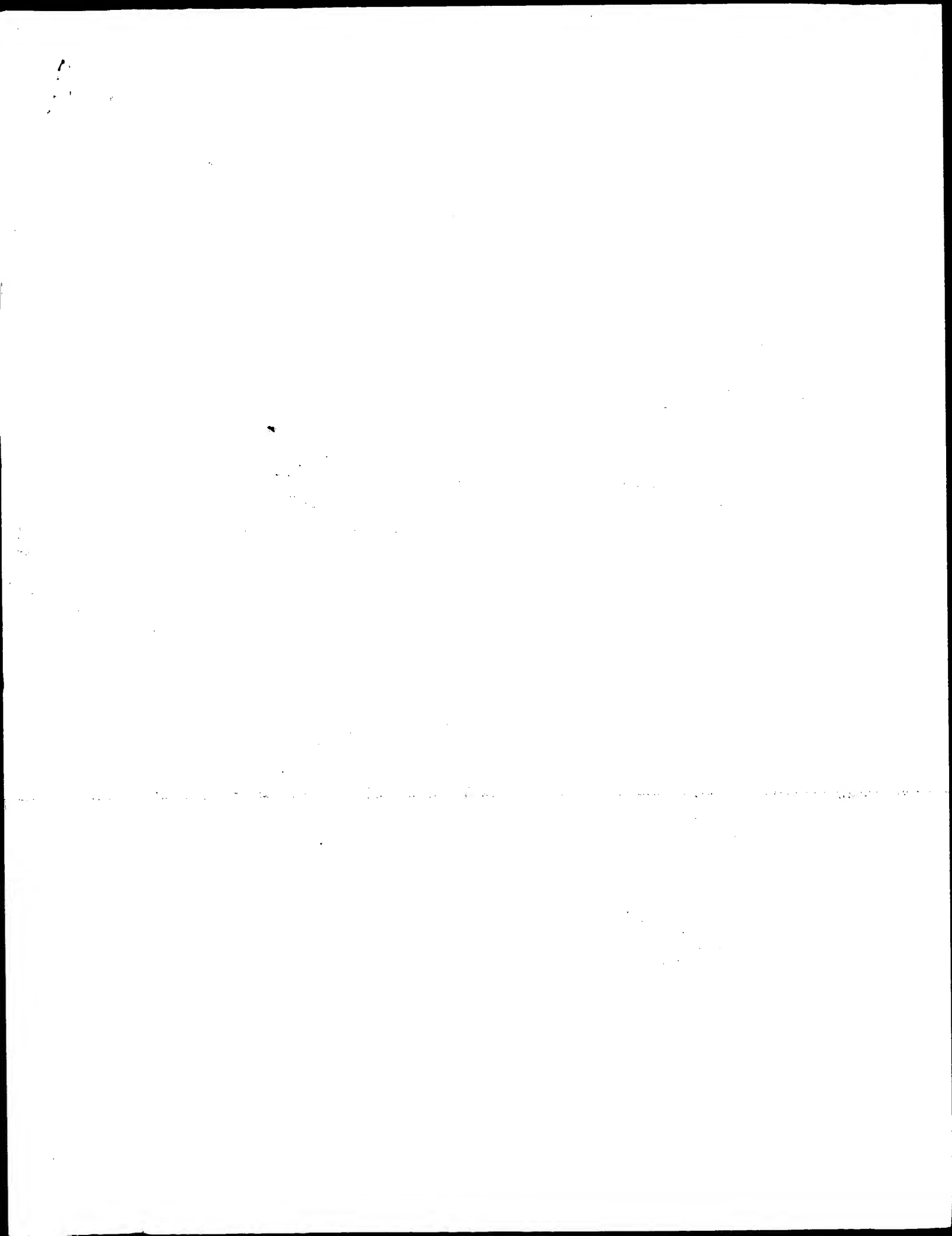
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 Site:2: Notif; Cloned unidirectionally. Primer: Oligo dt.
 library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"
 BASE COUNT 244 a 362 c 274 g 173 t
 ORIGIN

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 DB 147 CCTCGATCTGTGAGTGTGTGAGACCGACCGCGCTTCACCTTCACGCTATGAC 206
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 DB 207 TGTGAAGCTGCAAGGCTTTCTTCAAGCGGAGCATGAAGCGCAAGCGCTTCACTGCG 266
 OY 408 cccctccggaagggcgctcgtcagatcacccggaagaccgagcagtgccagggcctgc 467
 DB 267 CCTTC---AATGAGATTCGCCATCAACCAAGCAACCGCGCGACTGCCAGGCTTGC 323

OY 468 cgcctgcgcaagtgcctgagagcgagatgaaga-ggagatgataatgtccgac-gagg 525
 DB 324 CGGCTCAACCGCTGCTGAGACTCGCATGATGAACGGATTCAATCTCACAGACTGAGG 383
 OY 526 ccgtgagggagggcgggccttgatcaagcgaaagaagtgaaacggacggagcctcagc 585
 DB 384 AGTCAAGCTTAAGCGAGATGATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443
 OY 586 cactgagagtcagagggctgacagagagagcgagatgatacagggagctgagtgacg 645
 DB 444 GTCTAG---GCCCAAGCTGTCTGTGAGAGCAACAGACATCATCGCATCTGCTGATG 500
 OY 646 ctcaagatgaagaaaccttgacactaccctctcccaattcaagaatttcgcgtgcga 701
 DB 501 CCCACCAAGACTTACGACCCCACTATGCGCGACTTCGGGACTTCGCGCTTCA 556

Search completed: February 18, 2001, 19:19:59
 Job time: 17063 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 16, 2001, 16:49:16 ; Search time 124.29 seconds
(without alignments)
3633.206 Million cell updates/sec

Title: US-09-143-828-3

Perfect score: 2802
Sequence: 1 tgaattcgtggcctctgtg.....aaaaaaaaaaaaaaaaaaaaa 2802

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/2/1na/6.CONB.seq.*
4: /cgn2_6/ptodata/2/1na/PCRNUS.CONB.seq.*
5: /cgn2_6/ptodata/2/1na/Deckfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	278.8	10.0	2043 1	US-07-737-736B-6 Sequence 6, Appl
2	272.8	9.7	1399 1	US-07-737-736B-5 Sequence 5, Appl
3	170.6	6.1	1450 1	US-08-459-489-1 Sequence 1, Appl
4	170.6	6.1	1450 1	US-08-458-686-1 Sequence 1, Appl
5	170.6	6.1	1450 1	US-07-843-350C-1 Sequence 1, Appl
6	170.6	6.1	1450 4	PCR-US93-01559-1 Sequence 1, Appl
7	97.6	3.5	1898 1	US-08-342-411A-1 Sequence 1, Appl
8	97.6	3.5	1898 1	US-08-649-619B-1 Sequence 1, Appl
9	97.6	3.5	1898 1	US-08-649-619B-1 Sequence 1, Appl
10	97.6	3.5	2030 1	US-08-330-518-1 Sequence 1, Appl
11	97.6	3.5	2030 2	US-08-330-283-1 Sequence 1, Appl
12	97.6	3.5	2030 2	US-08-646-248-1 Sequence 1, Appl
13	97.6	3.5	2030 4	PCR-US95-13924-1 Sequence 1, Appl
14	97.2	3.5	1813 4	PCR-US94-12883-3 Sequence 3, Appl
15	91.4	3.3	2928 2	US-08-095-728B-3 Sequence 3, Appl
16	91.4	3.3	2928 2	PCR-US92-02320A-3 Sequence 3, Appl
17	91.4	3.3	2940 5	5171671-1 Patent No. 5171671
18	91.4	3.3	3036 1	US-08-306-691B-2 Sequence 52, Appl
19	91.4	3.3	3036 2	US-08-095-728B-1 Sequence 1, Appl
20	91.4	3.3	3036 4	PCR-US92-02320A-1 Sequence 1, Appl
21	91.4	3.3	3511 3	US-08-892-747-13 Sequence 13, Appl
22	89.8	3.2	704 2	US-08-592-383-5 Sequence 5, Appl
23	89.8	3.2	2940 2	US-08-592-383-1 Sequence 1, Appl
24	85.2	3.0	1959 1	US-08-342-411A-3 Sequence 4, Appl
25	85.2	3.0	1959 4	PCR-US94-12883-4 Sequence 3, Appl
26	83.8	2.9	2658 2	US-08-592-383-3 Sequence 3, Appl
27	80.8	2.9	1860 2	US-08-372-652-7 Sequence 7, Appl
28	80.8	2.9	1860 4	PCR-US95-16311-7 Sequence 7, Appl

29	79.6	2.8	1659 1	US-08-333-358-7 Sequence 7, Appl
30	79.6	2.8	1659 1	US-08-463-694-7 Sequence 7, Appl
31	79.6	2.8	1659 1	US-08-694-501-7 Sequence 1, Appl
32	77.6	2.8	2970 4	PCR-US92-06391-1 Sequence 2, Appl
33	77.6	2.7	1688 2	US-08-649-619B-2 Sequence 1, Appl
34	74.8	2.7	1649 2	US-08-466-130-1 Sequence 1, Appl
35	74.8	2.7	1649 4	PCR-US94-07266-1 Sequence 1, Appl
36	74.4	2.7	1576 5	5260432-1 Patent No. 5260432
37	74.4	2.7	2241 3	US-09-144-759-17 Sequence 17, Appl
38	74.4	2.7	2295 3	US-09-144-759-19 Sequence 19, Appl
39	74.4	2.7	2301 3	US-09-144-759-21 Sequence 21, Appl
40	73.2	2.6	2468 1	US-08-333-358-11 Sequence 11, Appl
41	73.2	2.6	2468 1	US-08-463-694-11 Sequence 11, Appl
42	73.2	2.6	2468 1	US-08-463-694-11 Sequence 11, Appl
43	72.6	2.6	1893 5	5438126-1 Patent No. 5438126
44	68.6	2.4	1677 2	US-08-372-652-14 Sequence 14, Appl
45	68.6	2.4	1677 4	PCR-US95-16311-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-07-737-736B-6
; Sequence 6, Application US/0737736B
; Patent No. 5260199
; GENERAL INFORMATION:
; APPLICANT: Deluca, Hector F.
; APPLICANT: Ross, Troy K.
; APPLICANT: Prahli, Jean M.
; TITLE OF INVENTION: Method Of Producing
; TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Carl R. Schwartz, Esq., c/o Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,736B
; FILING DATE: 19910730
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Carl R.
; REGISTRATION NUMBER: 29,437
; REFERENCE/DOCKET NUMBER: 96-296-2185-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 414-277-5715
; TELEFAX: 414-277-5774
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2043 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Double
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rat
; PUBLICATION INFORMATION:
; AUTHORS: Burnester, James K.
; AUTHORS: Wiese, Russell J.
; AUTHORS: Maeda, No. 5260199uyo
; AUTHORS: Deluca, Hector F.
; TITLE: Structure and regulation of the rat

; TITLE: 1,25-dihydroxyvitamin D3 receptor
 ; JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
 ; VOLUME: 85
 ; PAGES: 9499-9502
 ; DATE: December-1988
 ; US-07-737-736B-6

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Best Local Similarity	55.6%;	Pred. No. 4e-51;		
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Db	869	cttaatgtcaacggccgcatttgaggtgattcattgacgttccaaacacagcttttccacatgat	928
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RESULT 2
US-07-737-736B-5
: Sequence 5, Application file/07737736B

GENERAL INFORMATION:

APPLICANT: ROSS, TROY K.

APPLICANT: Pidal, Jean M.
TITLE OF INVENTION: Method of Producing

1	TITLE OF INVENTION:	1, 25-Dihydroxyvitamin D3 Receptor Protein
2	NUMBER OF SENTENCES:	6

CORRESPONDENCE ADDRESS:

STREET: 411 East Wisconsin Avenue

CITY: MILWAUKEE
STATE: Wisconsin

COUNTRY: U.S.A
ZTP. 53202

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0
;

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 115/07/7337 736B

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FILING DATE: 19910730

ATTORNEY/AGENT INFORMATION:

NAME: SCHWALZ, CALL K.
REGISTRATION NUMBER: 29,43

REFERENCE/DOCKET NUMBER: 96-296-2185-2

TELEPHONE: 414-277-5715
FEDERAL: 414-277-5774

INFORMATION FOR SEQ ID NO: 5

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SEQUENCE CHARACTERISTICS:
    LENGTH: 1399 base pairs

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TYPE: NUCLEIC ACID
STRANDEDNESS: double

TOPOLOGY: linear

HYPOTHETICAL: NO

ANAL SENSE: NO
ORIGINAL SOURCE:

ORGANISM: *Horrio saplens*

AUTHORS: Baker, Andrew R.

AUTHORS: Hughes, Mark

AUTHORS: Crisp, Tracey M.
Mangelsdorf, David J.

AUTHORS: Haussler, Mark R.
Pike, J. W.

AUTHORS: Shline, John

TITLE: Cloning and expression of full-length cDNA

TITLE: encoding human Vitamin D receptor

JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
 VOLUME: 85
 PAGES: 3294-3298
 DATE: May-1988
 US-07-737-736B-5

Query Match 9.7% Score 272.8; DB 1; Length 1399;
 Best Local Similarity 55.1%; Pred. No. 6.8e-50;
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 590 gtcgaagagagggcgctgtagatcacccgaaagagagagagagagagagagagag 649
 750 tcgagagagagggcgctgtagatcacccgaaagagagagagagagagagagagag 809
 650 tctggggagacgctgtagacacacacacacacacacacacacacacacacacacac 709
 810 tctctgagctgtagagggcgctgtagatcacccgaaagagagagagagagagagag 869
 710 tctgacagctgtagagggcgctgtagatcacccgaaagagagagagagagagagag 769
 870 gggggag 929
 770 ctgag 829
 930 aagggatcagcagcttgagagagagagagagagagagagagagagagagagagag 989
 830 caaag 889
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 1050 ttcag 1100
 950 ttccacatgag 1009
 1101 gaag 1160
 1010 gacgtgacaaag 1069
 1161 atgctgag 1220

Db 1070 GGAATGAGAGAGTGAATGCTGAGAGAGAGATGCTCTGCTATGCTGATC 1129
 Qy 1221 ttctccacagcccgaggtgctgtagacacgctggtgtagacagtgagagagaa 1280
 Db 1130 gctctccacagatgctctggtgtagacacgctggtgtagacagtgagagagaa 1189
 Qy 1281 ttctccacagatgctctggtgtagacacgctggtgtagacagtgagagagaa 1340
 Db 1190 ctgctccacagatgctctggtgtagacacgctggtgtagacagtgagagagaa 1249
 Qy 1341 ttctccacagatgctctggtgtagacacgctggtgtagacagtgagagagaa 1400
 Db 1250 ctgctccacagatgctctggtgtagacacgctggtgtagacagtgagagagaa 1309
 Qy 1401 cagcgcctgctgtagac 1418
 Db 1310 AAGGATGAGAGAGTGAATGCTGAGAGAGAGATGCTCTGCTATGCTGATC 1327

RESULT 3
 US-08-459-489-1
 : Sequence 1, Application US/08459489
 : Patent No. 568574
 : GENERAL INFORMATION:
 : APPLICANT: David D. Moore et al.
 : TITLE OF INVENTION: CAR RECEPTORS AND RELATED
 : TITLE OF INVENTION: MOLECULES AND METHODS
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Fish & Richardson
 : STREET: 225 Franklin Street
 : CITY: Boston
 : STATE: Massachusetts
 : COUNTRY: U.S.A.
 : ZIP: 02110-2804
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 : COMPUTER: IBM PS/2 Model 502 or 555X
 : OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
 : SOFTWARE: WordPerfect (Version 5.0)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/459,489
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/843,350
 : FILING DATE: February 26, 1992
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Paul T. Clark
 : REGISTRATION NUMBER: 30,162
 : REFERENCE/DOCKET NUMBER: 00786/126001
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (617) 542-5070
 : TELEFAX: (617) 542-8906
 : TELEX: 200154
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1450
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : US-08-459-489-1

Query Match 6.1%; Score 170.6; DB 1; Length 1450;
 Best Local Similarity 57.5%; Pred. No. 5.8e-28;
 Matches 327; Conservative 0; Mismatches 239; Indels 3; Gaps 1;

Qy 889 cctctgctccacagctgtagatgtagatgtagatgtagatgtagatgtagatgtagatg 948
 Db 739 cctctgctccacagctgtagatgtagatgtagatgtagatgtagatgtagatgtagatg 798
 Qy 949 ccaagatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 1008

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1450
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-458-686-1

Query Match      6.1%; Score 170.6; DB 1; Length 1450;
Best Local Similarity 57.5%; Pred. No. 5,8e-28;
Matches 327; Conservative 0; Mismatches 239; Indels 3; Gaps 1;

Db 799 CTAAGGACCTGCCGCTCTCCGTCCTCCATGGAAGACAGATCCCTTCAGAG 858
Qy 1009 gggccgcttgcagctgtgtcaactgagattcaacacagtggtcaacggagactgaa 1068
Db 859 GAGCAGCTGTGGAATCTGTACATCGTACTCAATACCACTTGTGTCCAAACACAA 918
Qy 1069 cctggagatgtgcccgcgtgtcctactgtcttggaagacatgcaggt--ggtcccaag 1125
Db 919 ACTTCCTCTGCGGCGCTCTTCGCTACACATGGAAGAGCCGCTGTGGGTTCCAG 978
Qy 1126 aacttctactggaccatgtctgaattccactacatgtctgaaagactgagctgcatg 1185
Db 979 TAGAGTTTGGAGTTGCTCTTTCCTTCACTTCACTGAAACACTGAAACACTGAGCTCCAG 1038
Qy 1186 aggaagatagtgtgtgtgtgcaagccatccctcttccccagaccgcccaggtgtgc 1245
Db 1039 AGCTGAGATGTGCTCTTGGCTGCAATGCGCCGCTGTCTCTGACGACCTGGAATTA 1098
Qy 1246 tgcagaccgcgtgtgtgaccagctgcaggaagcaattgcacattactctgaagtcctaca 1305
Db 1099 CCCAAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1158
Qy 1306 ttgaatgcaatcgcccgccagcctgtcctaggttcttctcctgaagatcagctatgc 1365
Db 1159 TCAAGGCCAGACGAGGAGGCGCCGCGGATCGGTTCTGTATGCAAGTGTCTAGGCTGCG 1218
Qy 1366 tcaccgagctcgccagcaatcaatgtctgacacacccagcgctgtcgtgacatcagadca 1425
Db 1219 TGCTGAGACTCGGAGCATTTAATGAGGCTTACGGGTTACCAATACGACATCCAGGAGCC 1278
Qy 1426 tacacccttgtctagcgcctcatgcag 1454
Db 1279 TGTCTGCATGATGCGGCTGCTCCAGGAG 1307

RESULT 4
US-08-458-686-1
; Sequence 1, Application US/08458686
; Patent No. 5710017
; GENERAL INFORMATION:
; APPLICANT: David D. Moore et al.
; TITLE OF INVENTION: CAR RECEPTORS AND RELATED
; TITLE OF INVENTION: MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM PS/2 Model 502 or 55SX
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,686
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/843,350
; FILING DATE: February 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/126001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1450
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-458-686-1

Query Match      6.1%; Score 170.6; DB 1; Length 1450;
Best Local Similarity 57.5%; Pred. No. 5,8e-28;
Matches 327; Conservative 0; Mismatches 239; Indels 3; Gaps 1;

Db 889 cctgtgcgcccacatggtgtgacatgtcaactactgttcaagagcatcagcttg 948
Db 739 CTCTGTCACACACTTCCGAGACATCAACATTTCTATGCTACGATGATCAAGTTTA 798
Qy 949 ccaaatcattctactactcaaggaattgccatcgagagaccagatctccctgtgaag 1008
Db 799 CTAAGGACCTGCCGCTCTCCGTCCTCCATGGAAGACCAAGATCCCTTCAGAG 858
Qy 1009 gggccgcttgcagctgtgtcaactgagattcaacacagtggtcaacggagactgaa 1068
Db 859 GAGCAGCTGTGGAATCTGTACATCGTACTCAATACCACTTGTGTCCAAACACAA 918
Qy 1069 cctggagatgtgcccgcgtgtcctactgtcttggaagacatgcaggt--ggtcccaag 1125
Db 919 ACTTCCTCTGCGGCGCTCTTCGCTACACATGGAAGAGCCGCTGTGGGTTCCAG 978
Qy 1126 aacttctactggaccatgtctgaattccactacatgtctgaaagactgagctgcatg 1185
Db 979 TAGAGTTTGGAGTTGCTCTTTCCTTCACTTCCATGAAACACTGAAACACTGAGCTCCAG 1038
Qy 1186 aggaagatagtgtgtgtgtgcaagccatccctcttccccagaccgcccaggtgtgc 1245
Db 1039 AGCTGAGATGTGCTCTTGGCTGCAATGCGCCGCTGTCTCTGACGACCTGGAATTA 1098
Qy 1246 tgcagaccgcgtgtgtgaccagctgcaggaagcaattgcacattactctgaagtcctaca 1305
Db 1099 CCCAAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1158
Qy 1306 ttgaatgcaatcgcccgccagcctgtcctaggttcttctcctgaagatcagctatgc 1365
Db 1159 TCAAGGCCAGACGAGGAGGCGCCGCGGATCGGTTCTGTATGCAAGTGTCTAGGCTGCG 1218
Qy 1366 tcaccgagctcgccagcaatcaatgtctgacacacccagcgctgtcgtgacatcagadca 1425
Db 1219 TGCTGAGACTCGGAGCATTTAATGAGGCTTACGGGTTACCAATACGACATCCAGGAGCC 1278
Qy 1426 tacacccttgtctagcgcctcatgcag 1454
Db 1279 TGTCTGCATGATGCGGCTGCTCCAGGAG 1307

RESULT 5
US-07-843-350C-1
; Sequence 1, Application US/07843350C
; Patent No. 5756448
; GENERAL INFORMATION:
; APPLICANT: David D. Moore et al.
; TITLE OF INVENTION: CAR RECEPTORS AND RELATED
; TITLE OF INVENTION: MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; OPERATING SYSTEM: IBM PS/2 Model 502 or 55SX
; SOFTWARE: WordPerfect (Version 3.30)

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RESULT 8

US-08-649-619B-1
Sequence 1, Application US/08649619B
Patent No. 5871916

GENERAL INFORMATION:

APPLICANT: NAKAMURA, YUSUKE
TITLE OF INVENTION: ECDN PROTEIN AND DNA
TITLE OF INVENTION: ENCODING THE SAME
NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLYNN, THIEL, BOUTELL &
ADDRESSEE: TANIS, P.C.
STREET: 2026 Rambling Road
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49008-1699

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 Inches, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM PC/XT/AT Compatible
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: WordPerfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/649,619B
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP6-226270

FILING DATE: 21-SEPT-1994
APPLICATION NUMBER: PCT/JP95/01909

FILING DATE: 21-SEPT-1995
ATTORNEY/AGENT INFORMATION:

NAME: Teriyence F. Chapman
REGISTRATION NUMBER: 32349

REFERENCE/DOCKET NUMBER: Furuya Case 1343
TELECOMMUNICATION INFORMATION:

TELEPHONE: (616) 381-1156
TELEFAX: (616) 381-5465

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1979
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:

ORGANISM: Homosapiens
IMMEDIATE SOURCE:

LIBRARY: Human mammary gland cDNA
LIBRARY: library

FEATURE:
NAME/KEY: CDS

LOCATION: 206..1591
IDENTIFICATION METHOD: experimental examination

US-08-649-619B-1

Query Match

Best Local Similarity 3.5%; Score 97.6; DB 2; Length 1979;
Matches 215; Conservative 0; Mismatches 174; Indels 3; Gaps 1;

QY 211 ctgacttgtaacatgtgagacagagctgtctccggaagcccaagtgtaacagcag 270

DB 378 CAGACTGGGTATCCAGATCCCGAAGGAAACAGACCCAGAAAGAGGCCAG 437

QY 271 atgaggaagctggagagtcacaaatctgcgtgtatgtgaggaagagcactgctatc 330

DB 438 CCCGAGATGCTGGGCAACGAGCTTCCGCTGTCTGTGGGAGCAAGGCCCGGCTTCC 497

QY 331 acttcaatgtcatatgtgaatgtgaagagcttttcagaggagccatgaacgca 390

DB 498 ACTACAGCTGCTACCTGGAAGGCTGCAGAGGCTTCTCCGGGCGAGTGTGCTCGTG 557

QY 391 acgcgcgcctgagtgccctccggaagggc---cctgagagataaccgggaagacc 447

DB 558 GTGGGGCCAGGCGCTATGCTGCGGGGTGGGGAACTGCGAGATGACGCTTTCATGC 617

QY 448 ggcgaagctgcagagcctgcgcctgcgaagtgcctggagagcgagctgaagagaga 507

DB 618 GCGGCAAGTCCAGAGTCCGCGCTCGCAAGTGCAGAGGAGGAGTGAAGGAGCAGT 677

QY 508 tgatcatgtccgcagggcgccgtagagagagcgagccttgatcaagcggaagaaagt 567

DB 678 GCGTCTTCTGAAGAACAGATCCGGAAGAGAAATTCGAAACAGCAGCAGCAGT 737

QY 568 aacgagagagactcagcagcctggagtgagcag 599

DB 738 CACAGTCACAGTCCAGTCACTGTGGGCGG 769

RESULT 9

US-08-330-518-1
Sequence 1, Application US/08330518
Patent No. 5607967

GENERAL INFORMATION:

APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine

APPLICANT: Rodan, Gideon
APPLICANT: Schmidt, Azriel

APPLICANT: Vogel, Robert
TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS

NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue

CITY: Rahway
STATE: New Jersey

COUNTRY: US
ZIP: 07065-0907

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/330,518
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Dolan, Catherine A.

REGISTRATION NUMBER: 36,502
REFERENCE/DOCKET NUMBER: 19316

TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4283

TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2030 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-330-518-1

Query Match

Best Local Similarity 3.5%; Score 97.6; DB 1; Length 2030;
Matches 215; Conservative 0; Mismatches 174; Indels 3; Gaps 1;

QY 211 ctgacttgtaacatgtgagacagagctgtctccggaagcccaagtgtaacagcag 270


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1 TELEPHONE: (908) 594-4283
2 TELEFAX: (908) 594-4720
3
4 INFORMATION FOR SEQ ID NO: 1:
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6 SEQUENCE CHARACTERISTICS:
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8 LENGTH: 2030 base pairs
9
10 TYPE: nucleic acid
11
12 STRANDEDNESS: single
13
14 TOPOLOGY: linear
15
16 MOLECULE TYPE: DNA (genomic)
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18 HYPOTHEetical: NO
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20 ANTI-SENSE: NO
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1008
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1010
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Query Match	3.58;	Score 97.6;	DB 2;	Length 2030;
Best Local Similarity	54.88;	Pred. No. 3e-12;		
Matches 215; Conservative	0;	Mismatches 174;	Indels 3;	Gaps 1;

[illegible]

RESULT 12
PCT-US95-13924-1
: Sequence 1, Application PC/TUS9513924
: GENERAL INFORMATION:
: APPLICANT: Friedman, Eitan
: APPLICANT: Holloway, M. Katharine
: APPLICANT: Rodan, Gideon
: APPLICANT: Rutledge, Su Jane
: APPLICANT: Schmidt, Azriel
: APPLICANT: Vogel, Robert
: TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merck & Co., Inc.
: STREET: 126 East Lincoln Avenue
: CITY: Rahway
: STATE: New Jersey
: COUNTRY: US
: ZIP: 07065-0907
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA: PCT/US95/13924

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1      FILING DATE:
2      CLASSIFICATION:
3      ATTORNEY/AGENT INFORMATION:
4      NAME: Ousg11sto, Carol S.
5      REGISTRATION NUMBER: 35,330
6      REFERENCE/DOCKET NUMBER: 19327 PCT
7      TELECOMMUNICATION INFORMATION:
8      TELEPHONE: (908) 594-3809
9      TELEFAX: (908) 594-4720
10     INFORMATION FOR SEQ ID NO: 1:
11     SEQUENCE CHARACTERISTICS:
12     LENGTH: 2030 base pairs
13     TYPE: nucleic acid
14     STRANDEDNESS: single
15     TOPOLOGY: linear
16     MOLECULE TYPE: DNA (genomic)
17     HYDROTHERMAL: NO
18     ANTI-SENSE: NO
19     PCT-US95-13924-1

```

Query Match	3.58;	Score 97.6;	DB 4;	Length 2030;
Best Local Similarity	54.88;	Pred. No. 3e-12;		
Matches 215; Conservative	0;	Mismatches 174;	Indels 3;	Gaps 1

Oy	211	ctgactctgtacacactgtgagagacacaaagctcttccctgtgaaagcccaagtgtcaaaagcag	270
Db	417	CAGACTGGGTATCCAGATGCCAGAAAGAACCCAGAGCCAGCCAGAAAGAGGCCACG	476
Oy	271	atgaggaagctgagaggtccccaactcgcgcgtgtatgtgtggagacaagggccactgtgctac	330
Db	477	CCCCGAGATGCTGGGGCAGAGGTTGGCGGTGTCTGGGGACAAAGGCTCCGGGCTTC	536
Oy	331	actcaatgtctcatgtgaaagtgaagatgcaagtgcaagggcttttcaggagggccatgtaaacga	380
Db	537	ACTCAACGTCCTACGCTGCGGAGAGGCTGCAGAGGGCTCTTCGCGCCGACAGTGTGCTGTG	586
Oy	391	acgcgcgcgtgaggtgtgcaccttcgcgaaagggcg---ccgtcgaaatcacccgcgaagacc	447
Db	537	GTGGGGCCAGGCGCTTATGCTCTGCGGGGGGTGGCGGAACCTGCCAGATGACGCTTTATGC	586
Oy	448	ggcagacagtgccagagccttcgcgcctctgcacagtgctcgtgagagcgcgcatgaagaaagga	507
Db	657	GGCGGAATGCCACAGAGGCCGCTGGCGCAAGTGCAGAGGAGCGGATGAGGAGCAGT	716
Oy	508	tgatcatgtccgagagggcgtgtgaggaagagcggggccttgatcaaacggaagaaagt	567
Db	717	GGCTCTCTTTGGAAGAACAGATCCGGGAAGAAGATTGGMAACACAGCAGCAGAGT	776
Oy	568	aaagcagaggaactcagccacttggagtgacg	599
Db	777	CACACTCACATTCGACAGTCACTCTTGGGGCCG	808

RESULT 13
PCT-US95-13931-1
Sequence 1, Application PC/TUS9513931
GENERAL INFORMATION:
APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
APPLICANT: Schmidt, Arzel
APPLICANT: Vogel, Robert
TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merck & Co., Inc.
STREET: 136 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13931
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Quagliato, Carol S.
REGISTRATION NUMBER: 35,330
REFERENCE/DOCKET NUMBER: 19316 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3809
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-13931-1

Query Match 3.5%; Score 97.6; DB 4; Length 2030;
Best Local Similarity 54.8%; Pred. No. 3e-12;
Matches 215; Conservative 0; Mismatches 174; Indels 3; Gaps 1;

QY 211 ctgaacttgtaactgtgaagacacagatctgttcttgaaagcccaagtgtcaacgag 270
DB 417 CAGACTGGGTCATCCAGATCCCGAAGAGACAGACGACGAGAAAGAGGGCCAG 476
QY 271 atgaggaagtcgagagcccaaatctgcgtgtatgttgaggaagagccactggtatc 330
DB 477 CCCCAGAGATGCTGGGACAGAGCTTGGCTGTGTGTGGGACAGGCTCCGGCTTCC 536
QY 331 acttcatgtcatgacatgtgaagatgacagatcttttcaggaagggccatgaacgca 390
DB 537 ACTCAACAGTGTGCTGAGTGGGAAGCGCAAGGCTTCTCCGCCACAGTGTGCTCCG 596
QY 391 agccgcgctgagtgccctcccgaaaggcg---ctgagagatcaccccgaaagccc 447
DB 597 GTGGGGCCAGCCCTATGCTGCGGGGTGGCGGAACCTGCAGATGACGCTTTCATGC 656
QY 448 gggagacagtcgagcctgagcctgagcaagtgccctgagagcgagcatgaagaagaga 507
DB 657 GGGGCAAGTCCAGCAAGTCCGGCTGGCAAGTGAAGAGGAGGAGGATGAGGACAGT 716
QY 508 tgatcatgtccgagagccgtgaggaagagcgagccttgatcaagcggaagaagagtg 567
DB 717 GCGTCTTCTGAAGAACAATCCGGGAAGAAGATTCGGAACAACAGCAGCAGAGACT 776
QY 568 aagcagagagagactcagccactggaagtcgag 599
DB 777 CACAGTCACAGTGCAGTCACTGTGGGGCCG 808

RESULT 14

PCT-US94-12883-3
Sequence 3, Application PC/TUS9412883
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR: COMPOSITIONS AND
METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas

COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12883
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,003
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA S. KITCHEN
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD154P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-12883-3

Query Match 3.5%; Score 97.2; DB 4; Length 1813;
Best Local Similarity 58.8%; Pred. No. 3.5e-12;
Matches 187; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 285 gttcccaaatctgcgtgtatgtggaagacagccactggtcttcaactcatgta 344
DB 229 GGCACAGAGCTTGGCCGTGTGTGGGACAGAGGCTTCCGCTTCCACTACAGTCTC 288
QY 345 acatgtgaagatgcaagagcttttcaggaagggccatgaacgcaagcccgctag 404
DB 289 AGCTCGAAGCTGCAAGAGGCTTCTCCGGCGCAGTGTGGTCCGTGGGGCCAGGCC 348
QY 405 tgccttcctcgaagagggcg---cctgagagatcacccggaagcccgagcagtc 461
DB 349 TATGCTTCCGCGGTGGGGAACCTGCAGATGACGCTTTCATGCGCGCAAGTGCAG 408
QY 462 gcttcgagcctgagcagtgctgagagcgagcatgaagaagagagatcatgtccgac 521
DB 409 CAGTCCCGGCTGCGCAAGTCCAGAGGAGGAGGATGAGGAGCAGTCTTCTTCTGAA 468
QY 522 gaggcgtgaggaagcgagcgcttgatcaagcggaagaagatgaacggaagagact 581
DB 469 GAACAGATCCCGAAGAAGATTCGGAACAGCAGCAGCAGAGTACAGTACAGTGC 528
QY 582 cagccactggaagtcgag 599
DB 529 CAGTCACTGTGGGGCCG 546

RESULT 15

US-08-095-7288-3
Sequence 3, Application US/080957288
Patent No. 5843642
GENERAL INFORMATION:
APPLICANT: DMITROVSKY, ETHAN
APPLICANT: WARBEL JR, RAYMOND P
APPLICANT: MILLER JR, WILSON H
APPLICANT: FRANKEL, STANLEY
TITLE OF INVENTION: METHODS FOR THE DETECTION AND

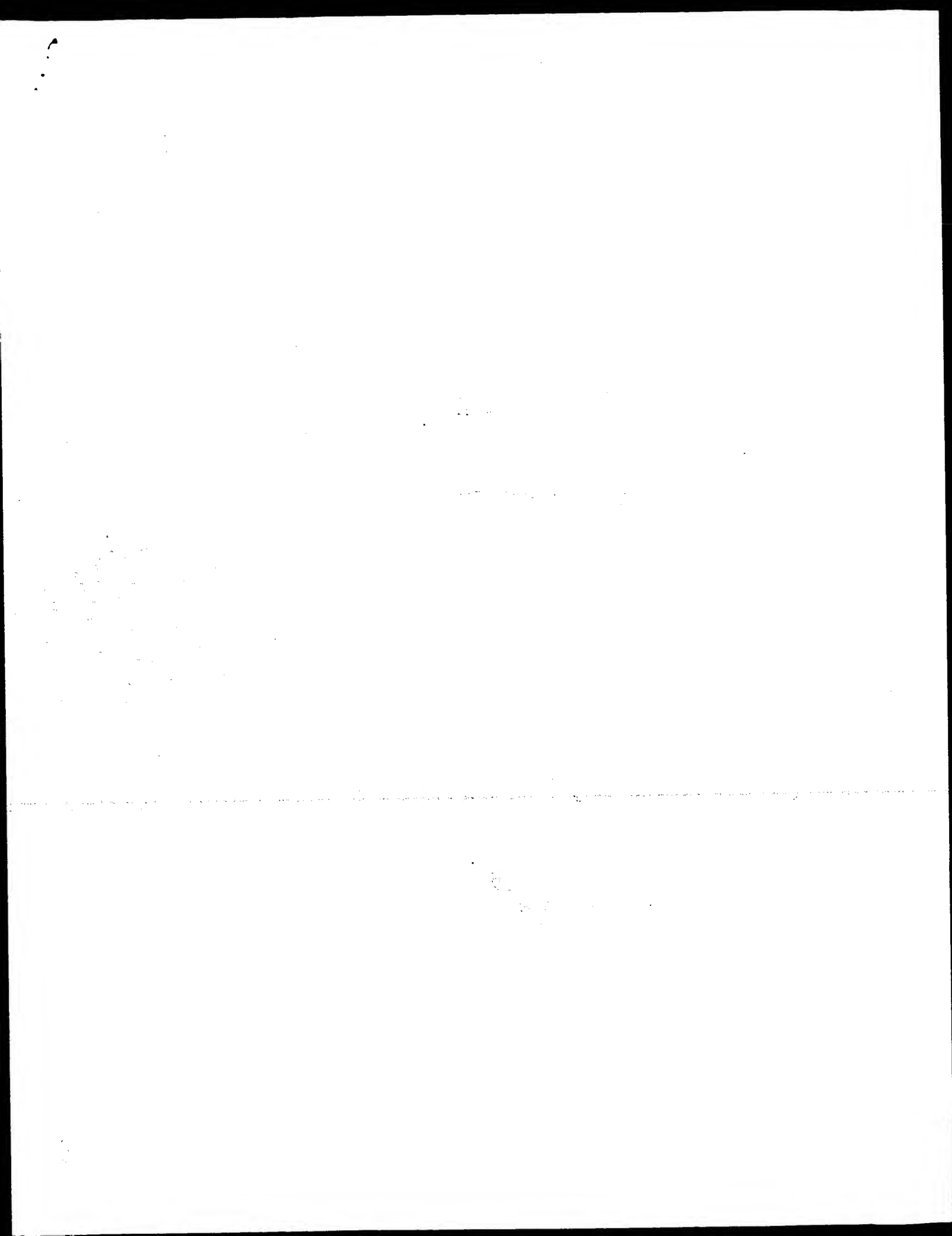
TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: COOPER & DUNHAM LLP
 STREET: 1185 AVENUE OF THE AMERICAS
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/095,728B
 FILING DATE: 21-JUL-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/673,838
 FILING DATE: 22-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: WHITE, JOHN P
 REGISTRATION NUMBER: 28,678
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2928 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 CLONE: hRAR ALPHA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 103..1488
 OTHER INFORMATION:
 US-08-095-728B-3

Query Match 3.3%; Score 91.4; DB 2; Length 2928;
 Best Local Similarity 50.8%; Pred. No. 7.1e-11;
 Matches 302; Conservative 0; Mismatches 281; Indels 12; Gaps 3;

QY 890 cctgctgcccacatgctgacatgcaacatgctgcaaaagcctcctcagcttgc 949
 DB 771 CCTCTGGACAGTTCAGTGAATCTCCACCAAGTCATCTTAAGACTGTGAGTTCG 830
 QY 950 caaagtcattctcctactcaggagacttgcacacacagcagagatcctcctgctgaagg 1009
 DB 831 CAAGCAGCTGCCCGCTTCCACCCTCACCCTCAGTCGCGACGACGATCACCCTCTCAAGC 890
 QY 1010 ggcgcgttcgagcgtgctgcaatcagattcaacacagcttcaacgcgagagactgaa 1069
 DB 891 TCCCTGCTGGACATCTGATCTGCGATTCGACGCGGTACACGCCCGCAGAGACAC 950
 QY 1070 ctggagagtg---ggcgcgtgctcctactgcttggagagacatgcaagtgcttcagga 1126
 DB 951 CATGACCTTCTGCGACGGGCTACCTGACCGGACCCAGATGCAACAGCTGCTTCGG 1010
 QY 1127 acttctactgagagcccatgctgaattcactacaatgctgaagaagctgcaagctgcatga 1186
 DB 1011 CCCCTCACCGACTGCTTTCCTTTCGCCACACGCTGCTGCCCTCGAGATGATGA 1070
 QY 1187 ggaagagatgctgctgag 1246
 DB 1071 TCGGAGAGAGGGGCTGCTCAAGCGCATCTGCTTCGCGAGACCGCAGAGACTGGA 1130
 QY 1247 gcaagacgcgctgctgagacagctgcaagagagagagagagagagagagagagagag 1306

DB 1131 GCACCCGACCGGCTGACATGCTGCAAGAGCCGCTGAGAGCCCTAAAGTCTACGT 1190
 QY 1307 tgaatgaatcgccccagcctgctcataggttcttccctgaagatcatgctatgct 1366
 DB 1191 GCGGAGAGGAGGCCGAGCGCCGCCACA-----TGTTCGCCAAGATCTTAATGAAT 1244
 QY 1367 caccgagcttcgagcatcaatgctcagacacccagcagctgct---gcgcatcagga 1423
 DB 1245 TACTGACCTCGAAGCATCAGCGCCCAAGGGGCTGAGCGGTGATCACGCTGAAGATGA 1304
 QY 1424 cataaaccttgcacgccccctatgagagaggtgttgcgcatcacaagtgagc 1478
 DB 1305 GATCCGCGGCTTCATGCGCCTCTCATCCAGAAATGTGGAGACTCAGAGGC 1359

Search completed: February 18, 2001, 16:49:45
 Job time: 8404 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: February 18, 2001, 16:54:40 ; Search time 211.71 Seconds

(without alignments)
4971.928 Million cell updates/sec

Title: US-09-143-828-3

Perfect score: 2802
Sequence: 1 tgaattcgtggtcgtctg.....aaaaaaaaaaaaaaaa 2802

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

N.Geneseq_36:*

- 1: /cgn2_2/gcgdata/geneseq/geneseq/NA1980.DAT.*
- 2: /cgn2_2/gcgdata/geneseq/geneseq/NA1981.DAT.*
- 3: /cgn2_2/gcgdata/geneseq/geneseq/NA1982.DAT.*
- 4: /cgn2_2/gcgdata/geneseq/geneseq/NA1983.DAT.*
- 5: /cgn2_2/gcgdata/geneseq/geneseq/NA1984.DAT.*
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- 9: /cgn2_2/gcgdata/geneseq/geneseq/NA1988.DAT.*
- 10: /cgn2_2/gcgdata/geneseq/geneseq/NA1989.DAT.*
- 11: /cgn2_2/gcgdata/geneseq/geneseq/NA1990.DAT.*
- 12: /cgn2_2/gcgdata/geneseq/geneseq/NA1991.DAT.*
- 13: /cgn2_2/gcgdata/geneseq/geneseq/NA1992.DAT.*
- 14: /cgn2_2/gcgdata/geneseq/geneseq/NA1993.DAT.*
- 15: /cgn2_2/gcgdata/geneseq/geneseq/NA1994.DAT.*
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- 19: /cgn2_2/gcgdata/geneseq/geneseq/NA1998.DAT.*
- 20: /cgn2_2/gcgdata/geneseq/geneseq/NA1999.DAT.*
- 21: /cgn2_2/gcgdata/geneseq/geneseq/NA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2802	100.0	2802	20 X56243	Human vitamin D re
2	2715.4	96.9	2850	20 X78808	Human nmr7-1 CDNA.
3	2702	96.4	3243	20 X59974	DNA encoding an in
4	2640.2	94.2	2810	20 X56242	Human vitamin D re
5	2586.2	92.3	3057	20 X59975	DNA encoding an in
6	2586.2	92.3	3093	20 X78807	Human nmr7 CDNA.
7	1866.6	66.6	2146	20 X07997	Human pregnane x r
8	1466.6	52.3	2068	20 X89080	Human steroid and
9	1442	50.7	1422	20 X59968	DNA encoding an in
10	1330.2	47.5	1374	20 X59967	DNA encoding an in
11	1305	46.6	1305	20 X59966	DNA encoding an in
12	425.2	15.2	644	20 X59972	SSO ID 12 of JP111

13	278.8	10.0	1960	19 V03129	CDNA encoding rat
14	278.8	10.0	2043	14 Q51425	Rat vitamin D rece
15	272.8	9.7	1382	20 X34789	Nucleotide sequenc
16	272.8	9.7	1463	20 X34788	Nucleotide sequenc
17	272.8	9.7	1574	20 X34793	Nucleotide sequenc
18	272.8	9.7	3510	20 Z07545	Human vitamin D re
19	272.8	9.7	4604	19 V41347	Human vitamin D re
20	271.2	9.7	1399	14 Q51424	Human vitamin D re
21	257	9.2	2191	17 T66499	Xenopus orphar rcc
22	236	8.4	1071	20 X16596	Rat vitamin D rece
23	236	8.4	3382	19 V18518	CDNA encoding rat
24	236	8.4	3382	20 X16606	Rat vitamin D rece
25	215	7.7	1534	20 X34790	Nucleotide sequenc
26	188.6	6.7	1404	20 X16597	Human vitamin D re
27	185.4	6.6	1404	19 V03130	CDNA encoding rat
28	181.6	6.5	1280	20 X60215	Mouse nuclear rece
29	172.2	6.1	1450	18 T92305	Constitutively act
30	170.6	6.1	1450	14 Q46131	Human CAR receptor
31	170.6	6.1	1450	20 X23994	Human CAR receptor
32	168.6	6.0	1361	20 X24003	Mouse CAR receptor
33	108.4	3.9	468	20 X80217	Mouse nuclear rece
34	97.6	3.5	1898	18 T79634	DNA encoding human
35	97.6	3.5	1979	17 T27616	Human foetal lung
36	97.6	3.5	2030	15 Q53132	Human recombinant
37	97.6	3.5	2030	17 T18996	Human steroid rece
38	97.6	3.5	2030	17 T30031	NMR receptor poten
39	97.2	3.5	1813	16 Q88760	Human ubiquitinous n
40	91.4	3.3	2928	13 Q29338	RAR-alpha gene. S
41	91.4	3.3	2928	20 V64991	Human RAR-alpha CD
42	91.4	3.3	2940	10 N90124	DNA of clone PHAR
43	91.4	3.3	3036	13 Q29334	myl/RAR-alpha fusi
44	91.4	3.3	3036	19 V20474	Human PML/RARalpha
45	91.4	3.3	3036	20 V64990	Human myl/RAR-alpha

ALIGNMENTS

RESULT 1

ID X56243 standard: CDNA: 2802 BP.

AC X56243;

DT 16-JUL-1999 (first entry)

DE Human vitamin D receptor related gamma 2 protein encoding CDNA.

KW Human; vitamin D receptor related protein; VDR; obesity; diabetes; anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia; hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; tumour; hyperproliferative skin disorder; hyperthyroidism; ss.

OS Homo sapiens.

PN WO9919354-A1.

PD 22-Apr-1999.

PF 31-AUG-1998; 98WO-SE01548.

PR 31-MAR-1998; 98SE-0001148.

PR 14-OCT-1997; 97SE-0003745.

PA (PHAA) PHARMACIA & UPJOHN AB.

PI Berkenstam A, Dahlberg M.

PI WPI: 1999-302508/25.

DR P-PSDB: Y09516.

PT New vitamin D receptor related (VDR) polypeptides, useful for treating obesity, diabetes, anorexia and rheumatoid arthritis

Db	1741	tcgagagagagagagtgctgcctcttcctttaaaaggccctcggtcgtcggtgagaaatccct	1800
Qy	1801	cagatcccaataaagtgcgaagtcgtgnaagggacaaagcgacaagataagccatctg	1860
Db	1801	cagatcccaataaagtgcgaagtcgtgnaagggacaaagcgacaagataagccatctg	1860
Qy	1861	gggtctatctgcccacataccaaagtttgctgcgtcttcctgaagcttttcaatctgcacctta	1920
Db	1861	gggtctatctgcccacataccaaagtttgctgcgtcttcctgaagcttttcaatctgcacctta	1920
Qy	1921	atagatctgctcccaacttcaccactggtctccctccctccctccagagctcctctgtggctc	1980
Db	1921	atagatctgctcccaacttcaccactggtctccctccctccctccagagctcctctgtggctc	1980
Qy	1981	aaaggtctgtatcgaatcgcgcaggtgcatagtgaatactgtggtgagttccctctagaagagatga	2040
Db	1981	aaaggtctgtatcgaatcgcgcaggtgcatagtgaatactgtggtgagttccctctagaagagatga	2040
Qy	2041	agccaaagagagccctgcgacacaaatgtccgaagaagcttgagacatctacatctccggccacatcat	2100
Db	2041	agccaaagagagccctgcgacacaaatgtccgaagaagcttgagacatctacatctccggccacatcat	2100
Qy	2101	tcctgtgctctgtgataccatttgnaacatactatataagacatgtgaataagtgatgcctgct	2160
Db	2101	tcctgtgctctgtgataccatttgnaacatactatataagacatgtgaataagtgatgcctgct	2160
Qy	2161	gggtgtatcacagcatctgaatcagataaagaatacctctgaagctcacagaagttatagttaaaata	2220
Db	2161	gggtgtatcacagcatctgaatcagataaagaatacctctgaagctcacagaagttatagttaaaata	2220
Qy	2221	acaaacacgaacacacaaacaaatcttgatcacaaagagagaaataataagtcgacaaagaacgcg	2280
Db	2221	acaaacacgaacacacaaacaaatcttgatcacaaagagagaaataataagtcgacaaagaacgcg	2280
Qy	2281	acaaagagaaattccctctgtgtgatagtgcgaagctgtgatagtgnaagcacatgtgtgaaccaaagatga	2340
Db	2281	acaaagagaaattccctctgtgtgatagtgcgaagctgtgatagtgnaagcacatgtgtgaaccaaagatga	2340
Qy	2341	aggtctcccgagagaaatgagatctgtgaagagacaaagggacaaacatgcaagctgtgagtgtgcgtg	2400
Db	2341	aggtctcccgagagaaatgagatctgtgaagagacaaagggacaaacatgcaagctgtgagtgtgcgtg	2400
Qy	2401	tgctgtgattctgtgtgaggtacagtcctgtttgcacactgataagggcctgtggctgttctcccg	2460
Db	2401	tgctgtgattctgtgtgaggtacagtcctgtttgcacactgataagggcctgtggctgttctcccg	2460
Qy	2461	ggctcgagaaatgtctgtgtgtctgtgacaaaggtataagcgcgaacatacgaattaaacacacg	2520
Db	2461	ggctcgagaaatgtctgtgtgtctgtgacaaaggtataagcgcgaacatacgaattaaacacacg	2520
Qy	2521	gagaaagaaacacatacagatcgacacttaattctcgtgtacaacatactatctccaaagcttaaa	2580
Db	2521	gagaaagaaacacatacagatcgacacttaattctcgtgtacaacatactatctccaaagcttaaa	2580
Qy	2581	gggtatctgaagtgctgcctgcctgtgttatagacactgtgagtaaaaaattttttgtgacattc	2640
Db	2581	gggtatctgaagtgctgcctgcctgtgttatagacactgtgagtaaaaaattttttgtgacattc	2640
Qy	2641	cacaaatatactcttatataaaggaattcccaacactgaagaacttttttggaagaagtgcg	2700
Db	2641	cacaaatatactcttatataaaggaattcccaacactgaagaacttttttggaagaagtgcg	2700
Qy	2701	cctgtggttaatgtccaatcgaagcgaaaggaattcaatatgttaactttgtgctaaaaaa	2760
Db	2701	cctgtggttaatgtccaatcgaagcgaaaggaattcaatatgttaactttgtgctaaaaaa	2760
Qy	2761	aaa 2802	
Db	2761	aaa 2802	
RESULT	2		

ID	X78808
XX	X78808 standard; cDNA; 2850 BP.
AC	X78808:
DT	06-SEP-1999 (first entry)
DE	Human nNR7-1 cDNA.
XX	nNR7; nNR7-1 nuclear trans-acting receptor protein; human; regulator;
KW	identification; downstream target gene; cell proliferation;
KW	cell development; ss.
OS	Homo sapiens.
FT	Key Location/Qualifiers.
FT	CDS 104..1525
FT	/tag= A.
FT	/product= "nNR7-1"
PN	WO9931129-A1.
PD	24-JUN-1999.
XX	PF 11-DEC-1998; 98WO-US26364.
PR	14-OCT-1998; 98US-0104251.
PR	12-DEC-1997; 97US-0069401.
PA	(MERI) MERCK & CO INC.
PI	Chen F;
DR	WPI; 1999-405024/34.
DR	P-PsDB; Y25411.
PT	DNA encoding human nuclear receptors nNR7 and nNR7-1
PS	Claim 28; Fig 4A-C; 80pp; English.
CC	This invention describes the isolation of the novel human nuclear
CC	receptors nNR7 or nNR7-1. The nNR7 and nNR7-1 proteins are useful in
CC	the identification of downstream target genes and ligands regulating its
CC	activity. The nuclear receptor is involved in the regulation of in vivo
CC	cell proliferation and/or cell development. The nNR7 and nNR7-1
CC	polynucleotides, expression vectors and host cells are useful for the
CC	recombinant production of the protein.
SO	Sequence 2850 BP; 691 A; 736 C; 787 G; 636 T; 0 other;
Query Match	96.9%; Score 2715.4; DB 20; Length 2850;
Best Local Similarity	99.7%; Pred. No. 0;
Matches 2741; Conservative	0; Mismatches 6; Indels 2; Gaps 2
QY	9 tgggctcgttggttgcgttcgtcgagccccctggaggccaagagacgcgatgacagtc 68
DB	
54	tggccctcgttggttagtgcgtgcag-cccctgaaggccaagagcacgcagcatgacagtc 112
QY	accaggaactcaccaactccaaggaggggtccctcagaagacacctgccataccctgcacagt 128
DB	
113	accaggaactcaccaactccaaggaggggtccctcagaagacacctgccataccctgcacagt 172
QY	gctgcgctgagttggcttcaaaccatccaaagagggcccaagaaacattggaagtgaag 188
DB	
173	gctgcgctgagttggcttcaaaccatccaaagagggcccaagaaacattggaagtgaag 232
QY	caccaagaagaagctggaacatctgcacttgttacaactgtaggaacacagatgtgtcc 248
DB	
233	caccaagaagaagctggaacatctgcacttgttacaactgtaggaacacagatgtgtcc 292
QY	ggaaaagcccggttcaaacagatatgaggaagtgcggaagtcgccaaatctgcctgtatgt 308
DB	

Db 293 ggaagaccagatgtaacagcagatgaggaagtcggaaggtccccaatctgcgtgtatgt 352
QY 309 gggagcaagagccatggtctatcatctcaatgtcatgtgagagatgcaagagcttt 368
Db 353 gggagcaagagccatggtctatcatctcaatgtcatgtgagagatgcaagagcttt 412
QY 369 ttcaagagagccatgtaaaacagcccgctgagagtgcccttcctcggaagagcgctgc 428
Db 413 ttcaagagagccatgtaaaacagcccgctgagagtgcccttcctcggaagagcgctgc 472
QY 429 gagatcaccccggaagagcccgctgagagtgcccttcctcggaagagcgctgc 488
Db 473 gagatcaccccggaagagcccgctgagagtgcccttcctcggaagagcgctgc 532
QY 489 agcggtcatgaaagagagatgatactgctccagcagcgctgagagagcgagcgcttcg 548
Db 533 agcggtcatgaaagagagatgatactgctccagcagcgctgagagagcgagcgcttcg 592
QY 549 atcaagcggaagaaagatgaaacagcagagagctcaagccactgagagtgcaagggctga 608
Db 593 atcaagcggaagaaagatgaaacagcagagagctcaagccactgagagtgcaagggctga 652
QY 609 gagagagcagcgagatgatacagagagagtgatgagcgtctcagatgaaacacttgacac 668
Db 653 gagagagcagcgagatgatacagagagagtgatgagcgtctcagatgaaacacttgacac 712
QY 669 acccttcctccattcaaaagatctcccgctgagagagtgcttaagcagtgctgagatgtg 728
Db 713 acccttcctccattcaaaagatctcccgctgagagagtgcttaagcagtgctgagatgtg 772
QY 729 ccagagatctctcgagagcccatctgagagagagagctgcaagtgagagccagagtcgga 788
Db 773 ccagagatctctcgagagcccatctgagagagagagctgcaagtgagagccagagtcgga 832
QY 789 gatctgtgctcttggagaggtctctctgagagtgctgagagagagagagagagagagag 848
Db 833 gatctgtgctcttggagaggtctctctgagagtgctgagagagagagagagagagagag 892
QY 849 tacaaaaccccgagcagagagtgctgagagagagagagagagagagagagagagagag 908
Db 893 tacaaaaccccgagcagagagtgctgagagagagagagagagagagagagagagagag 952
QY 909 gagatgtcaaacctcatgttcaaaagagcatcagctttgcgaagatcatctctacttc 968
Db 953 gagatgtcaaacctcatgttcaaaagagcatcagctttgcgaagatcatctctacttc 1012
QY 969 agggactgtcccatcgag 1028
Db 1013 agggactgtcccatcgag 1072
QY 1029 caactgtgagatcaaacagatgttcaacgagagagagagagagagagagagagagagag 1088
Db 1073 caactgtgagatcaaacagatgttcaacgagagagagagagagagagagagagagagag 1132
QY 1089 tctcaactgttggag 1148
Db 1133 tctcaactgttggag 1192
QY 1149 aaatcccatcatcatgctgaaagagagagagagagagagagagagagagagagagagag 1208
Db 1193 aaatcccatcatcatgctgaaagagagagagagagagagagagagagagagagagagag 1252
QY 1209 gcatctccctctctcccaagagcagagtgctgagagagagagagagagagagagagagag 1268
Db 1253 gcatctccctctctcccaagagcagagtgctgagagagagagagagagagagagagagag 1312
QY 1269 ctgag 1328
Db 1313 ctgag 1372
QY 1329 gctcatag 1388
Db 1373 gctcatag 1432

QY 1389 gctcaagacacacccagcgtctgctgcatcagagagagagagagagagagagagagagag 1448
Db 1433 gctcaagacacacccagcgtctgctgcatcagagagagagagagagagagagagagagag 1492
QY 1449 atgcaagagatgtctcgcatcacaagagagagagagagagagagagagagagagagag 1508
Db 1493 atgcaagagatgtctcgcatcacaagagagagagagagagagagagagagagagagag 1552
QY 1509 gagagcag 1568
Db 1553 gagagcag 1612
QY 1569 gccaaagacag 1628
Db 1613 gccaaagacag 1672
QY 1629 ggtcagcatctccatcag 1688
Db 1673 ggtcagcatctccatcag 1732
QY 1689 tgaagcacaag 1748
Db 1733 tgaagcacaag 1792
QY 1749 gcaaggtgctcccttccttcaaaagagagagagagagagagagagagagagagagagag 1808
Db 1793 gcaaggtgctcccttccttcaaaagagagagagagagagagagagagagagagagagag 1852
QY 1809 actaaagtgctcaagagtgag 1868
Db 1853 actaaagtgctcaagagtgag 1912
QY 1869 gcccaatcacag 1928
Db 1913 gcccaatcacag 1972
QY 1929 gttcccaatcccatcctgctcccttccttccttccttccttccttccttccttccttc 1988
Db 1973 gttcccaatcccatcctgctcccttccttccttccttccttccttccttccttccttc 2032
QY 1989 taactacag 2048
Db 2033 taactacag 2092
QY 2049 ggcctgcaacacatgctgag 2108
Db 2093 ggcctgcaacacatgctgag 2152
QY 2109 tctgcatcattgaaacacatattaaagacatgagatagagagagagagagagagagagag 2168
Db 2153 tctgcatcattgaaacacatattaaagacatgagatagagagagagagagagagagagag 2212
QY 2169 cagcatgacatcagatagatcctgagctcagagagagagagagagagagagagagagag 2228
Db 2213 cagcatgacatcagatagatcctgagctcagagagagagagagagagagagagagagag 2272
QY 2229 aaaaacaaacattgagatcaaaagagagagagagagagagagagagagagagagagag 2288
Db 2273 aaaaacaaacattgagatcaaaagagagagagagagagagagagagagagagagagagag 2331
QY 2289 ttccctctgtgagatgag 2348
Db 2333 ttccctctgtgagatgag 2391
QY 2349 gagagacagatcgtctag 2408
Db 2393 gagagacagatcgtctag 2451
QY 2409 ttggtgag 2468
Db 2453 ttggtgag 2511

QY	2469	tcctgggtatgctctctggaacaagcgaacgtctgacacatctggttaaaacaacccgagagaga	2538
Db	2512	tgcgcgggtatgctctctggaacaagcgaacgtctgacacatctggttaaaacaacccgagagaga	2571
QY	2539	ccattacatgcaacctatatacttcgtgcacacatctcacaagctaaagagatgca	2588
Db	2572	ccattacatgcaacctatatacttcgtgcacacatctcacaagctaaagagatgca	2631
QY	2589	aagtcgcctgctctgttatagccaactctggagataaaattttttgcatttcacaaatt	2648
Db	2632	aagtcgcctgctctgttatagccaactctggagataaaattttttgcatttcacaaatt	2693
QY	2649	atacttatataaagcattccacacctaaagacatgttttgggaaaatgtagccctgggt	2708
Db	2692	atacttatataaagcattccacacctaaagacatgttttgggaaaatgtagccctgggt	2751
QY	2709	taaatgtaaatcaagaagaaaagaaatataatgtaacttttggcgctaa	2757
Db	2752	taaatgtaaatcaagaagaaaagaaatataatgtaacttttggcgctaa	2800

RESULT 3

ID	X59974	standard; DNA; 3243 bp.
XX		
AC	X59974;	
XX		
DT	04-AUG-1999	(first entry)
XX		
DE	DNA encoding an intranuclear receptor protein.	
XX		
KN	Human; intranuclear receptor protein; drug development; diagnosis; treatment; ss.	

OS Homo sapiens.
XX JP1127872-A.
XX
XX 18-MAY-1999.
XX
XX 07-AUG-1998; 98JP-0224172.
XX
XX 11-AUG-1997; 97JP-0230335.
XX
XX (NISB) JAPAN TOBACCO INC.
XX
XX WPI: 1999-350330/30.
XX
XX P-PSDB: Y15936.
XX
XX
XX New intranuclear receptor protein - useful for drug development and
XX diagnosis and treatment of disease
XX
XX
XX Claim 10: Page 32-35; 38pp; Japanese.
XX
XX The present sequence encodes a human intranuclear receptor protein.
XX The nucleic acid sequence was isolated from a human adult cDNA
XX library using a swainfish ANO23 derived probe. The protein can
XX be used for the development of drugs and diagnosis and treatment
XX of various diseases.
XX
XX Sequence 3243 BP; 838 A; 806 C; 862 G; 737 T; 0 other;

Query Match	96.4%	Score 2703	DB 20	Length 3243
Best Local Similarity	99.8%	Pred. No. 0		
Matches 2716; Conservative	0	Mismatches 5	Indels 1	Gaps 1

QY	36	ccccctgagcgcaagagacagacatgacatcaccaggaatcaccacattcaagagagggg	95
Db	320	ccccctgagcgcaagagacagacatgacatcaccaggaatcaccacacattcaagagagggg	379
QY	96	tccctcagagcacctgccaataccccctgcaacagctgctcgcgcttgaggttggcttcaaacat	155

[illegible]

XX	JP1127872-A.
PN	
XX	
PD	18-MAY-1999.
XX	
PF	07-AUG-1998; .98UP-0224172.
XX	
PR	11-AUG-1997; 97JP-0230335.
XX	
PA	(NISB) JAPAN TOBACCO INC.
DR	WPI; 1999-350330/30.
DR	P-PsDB; Y16035.
XX	
PT	New intranuclear receptor protein - useful for drug development and diagnosis and treatment of disease
XX	
PS	Claim 10; Page 35-37; 38pp; Japanese.
XX	
CC	The present sequence encodes a human intranuclear receptor protein.
CC	The nucleic acid sequence was isolated from a human adult cDNA
CC	library using a swellfish ANO23 derived probe. The protein can
CC	be used for the development of drugs and diagnosis and treatment
SQ	of various diseases.
	Sequence 3057 BP; 792 A; 751 C; 813 G; 701 T; 0 other;
Query Match	92.3%; Score 2586.2; DB 20; Length 3057;
Best Local Similarity	99.5%; Pred. No. 0;
Matches 2605; Conservative +; 0; Mismatches 13; Indels 1; Gaps	
OY	139 atttgcttcaaccatccaaagagccccagaagacaactgtgagttagaccacgaaga 198
Dd	237 acttacccaacagcagctccaagaggcccacagaagaacctgtgagttagaccacgaaga 296
OY	199 gctggacaaccatgtgactttgtacaactgtgagacaagaagtcgtctctcgaaaagccca 255
Dd	297 gctggacaaccaatgtactatttgtacactgtgagacacagaagtcgtctctcgaaaagccca 356
OY	259 gtgtcaaacgcagataaggaagctcggaagctcccaaatctgcgcgtgtatgttggggacaag 318
Dd	357 gtgtcaaacgcagataaggaagctcggaagctcccaaatctgcgcgtgtatgttggggacaag 410
OY	319 ccactgtgtcatcactttcatactgtcacatgtgtgaagatgcaagagcgttttccagagaggg 378
Dd	417 ccactgtgtcatcactttcatactgtcacatgtgtgaagatgcaagagcgttttccagagaggg 476
OY	379 ccattgaacgcgaagccccgcgtgtgaggtgtgcccttccggaagggcgccctgtgatcaagcga 438
Dd	477 ccattgaacgcgaagccccgcgtgtgaggtgtgcccttccggaagggcgccctgtgatcaagcga 536
OY	439 ggaagagccccgcgcgaactgtccagagccctctgcgcctctgcgaagctgccttgagagcgacga 498
Dd	537 ggaagagccccgcgcgaactgtccagagccctctgcgcctctgcgaagctgccttgagagcgacga 596
OY	499 agaaagagatatatcatgtccgacagacgcgtgtgagagagagcgagccttgcataacgcga 558
Dd	597 agaaagagatatatcatgtccgacagacgcgtgtgagagagagcgagccttgcataacgcga 656
OY	559 agaaaaagtgaaacgcgaacgcggcctaagccactgtggaatgtgcgggggtctgcacagaagagcagc 618
Dd	657 agaaaaagtgaaacgcgaacgcggcctaagccactgtggaatgtgcgggggtctgcacagaagagcagc 716
OY	619 ggatgatgatcatagagagacgtgatgagacgctcagatgtaaaacctttgacatacattctccc 678
Dd	717 ggatgatgatcatagagagacgtgatgagacgctcagatgtaaaacctttgacatacattctccc 776
OY	679 attccaagaatttcgcgcgtccgcacaggggtgttgtagcagctgtcgcagattccagaagtctc 738
Dd	777 attccaagaatttcgcgcgtccgcacaggggtgttgtagcagctgtcgcagattccagaagtctc 836
OY	739 tgcacggcccccttcgagaggaagaaactctccaaagtgtgaagccaggtcccgaaagaagatctgtgct 798

|||||
Db 837 tgcagcccccacgaggaagagagctgcacaaagtgcagagctccggagaaatctgtgct 896
QY 799 ctttgaaggtctctctgcaagctgcgggggagagatgcagagctgcggagaaacaaacccc 858
Db 897 ctttgaaggtctctctgcaagctgcgggggagagatgcagagctgcggagaaacaaacccc 956
QY 859 cagccgagacgtgcgggaaagaaagaaatctctccctgctgcacccacaaatgctgacatgtcaaa 918
Db 957 cagccgagacgtgcgggaaagaaagaaatctctccctgctgcacccacaaatgctgacatgtcaaa 1016
QY 919 cctacaatgttcaaaagacatcaatcaagcttgcacaaagtcatctcctaattcaggagacttgc 978
Db 1017 cctacaatgttcaaaagacatcaatcaagcttgcacaaagtcatctcctaattcaggagacttgc 1076
QY 979 ccatcagagagacagatctccctcctgcggaaggggagccgcttgcagagtggtgtcaaacagat 1038
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QY 1039 tcaaacacagtgctcaaacgagagagactgcggaacctgcggaagtgctgcagcgtctcctaactgt 1098
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QY 1099 tggaaagacatgcagagtggtctccagcaactctcactgcggaacacatgcctgaaatccact 1158
Db 1197 tggaaagacatgcagagtggtctccagcaactctcactgcggaacacatgcctgaaatccact 1256
QY 1159 acaatgctgaaagaaagctgcagcgtgcatagtgagagaaatgctgtgtgtgcagagcaactccc 1218
Db 1257 acaatgctgaaagaaagctgcagcgtgcatagtgagagaaatgctgtgtgtgcagagcaactccc 1316
QY 1219 tctctcccccagacacgcccagagtgctgctgcagacacgctgctgagacacagctgcagagagc 1278
Db 1317 tctctcccccagacacgcccagagtgctgctgcagacacgctgctgagagacacgctgcagagagc 1376
QY 1279 aatctgcacatcaatctctgaaggtctcaatctgaatgcaatgcgcgcacagcctgcctcaatgct 1338
Db 1377 aatctgcacatcaatctctgaaggtctcaatctgaatgcaatgcgcgcacagcctgcctcaatgct 1436
QY 1339 tctgttctctgaagatcaatgagctatgctcaacgagctgcagacacatcaatgctgcagacaa 1398
Db 1437 tctgttctctgaagatcaatgagctatgctcaacgagctgcagacacatcaatgctgcagacaa 1496
QY 1399 cccagagcgtgcctgcacatccagagacatacaccccttgcctgcagccctcagcagagaggt 1458
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QY 1459 tgttcgacatcaacagtgagctgcagcgtgcctgcctgtggtgacacaccccgagagagagcaca 1518
Db 1557 tgttcgacatcaacagtgagctgcagcgtgcctgcctgtggtgacacaccccgagagagagcaca 1616
QY 1519 gacccagagacccctctgagcgcgcacaccccgaggagaaagatgagacatgcgcagagagc 1578
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QY 1579 gacaaagccctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcct 1638
Db 1677 gacaaagcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcctgcct 1736
QY 1639 cctcagagaaagacatggtgcctcccccacacccagatcagctgctgagagagtgaaagcaca 1698
Db 1737 cctcagagaaagacatggtgcctcccccacacccagatcagctgctgagagagtgaaagcaca 1796
QY 1699 gactcttaagtgagagtgagacatgagctgagctgagctgagctgagctgagctgagctgagctg 1758
Db 1797 gactcttaagtgagagtgagacatgagctgagctgagctgagctgagctgagctgagctgagctg 1856
QY 1759 ccttcccttttaaaagacccctgctgctgcgggagaaatccctcagatccacataaagtgct 1818
Db 1857 ccttcccttttaaaagacccctgctgctgcgggagaaatccctcagatccacataaagtgct 1916
QY 1819 caaggtgtggaagagacaaagcgaacaaagataagcgaatctggtgtctatgcacacatac 1878
|||||

Db 1917 caaggtgtggaagagacaaagcgaacaaagataagcgaatctggtgtctatgcacacatac 1976
QY 1879 ccaaggtgtgtctctcctgcagagctcttctcaatgctacacctaataagctctgtctccact 1938
Db 1977 ccaaggtgtgtctctcctgcagagctcttctcaatgctacacctaataagctctgtctccact 2036
QY 1939 tcccaactcgtctccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1998
Db 2037 tcccaactcgtctccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 2096
QY 1999 caggtgcagatgagatctgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 2058
Db 2097 caggtgcagatgagatctgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 2156
QY 2059 aaatgtcaagaagctgtgcagatgacatccatccgcgcacatcattctgtctcctgcaccca 2118
Db 2157 aaatgtcaagaagctgtgcagatgacatccatccgcgcacatcattctgtctcctgcaccca 2216
QY 2119 ttggaacacatctaaagcactgataaagtgagcctgcctgctggtgtatcacagatctgac 2178
Db 2217 ttggaacacatctaaagcactgataaagtgagcctgcctgctggtgtatcacagatctgac 2276
QY 2179 tcaagataaagctcctgcagcctcagacagatcttaagttaaaacaaacaaacaaacaaacaaac 2238
Db 2277 tcaagataaagctcctgcagcctcagacagatcttaagttaaaacaaacaaacaaacaaacaaac 2336
QY 2239 aatttgatcaaaagagagaaatcatatagtgagacaaagcagcacaagagaaattccctgtg 2298
Db 2337 aatttgatcaaaagagagaaatcatatagtgagacaaagcagcacaagagaaattccctgtg 2395
QY 2299 tggatgctgagcctgtgagctgcagagcactgcgtgacccaaagtgaaggttcccgagagacatga 2358
Db 2396 tggatgctgagcctgtgagctgcagagcactgcgtgacccaaagtgaaggttcccgagagacatga 2455
QY 2259 gtctgtgag 2418
Db 2456 gtctgtgag 2515
QY 2419 taagtctgcttgcacacttgatctgagcctgcgtggtgtgtctcctgcgggagagagagagagat 2478
Db 2516 taagtctgcttgcacacttgatctgagcctgcgtggtgtgtctcctgcgggagagagagagagat 2575
QY 2479 gtctgtgag 2538
Db 2576 gtctgtgag 2635
QY 2539 gcaactataatttctgtgtacacatctatctcaaaagctaaagaggtatgaaagtgcctgc 2598
Db 2636 gcaactataatttctgtgtacacatctatctcaaaagctaaagaggtatgaaagtgcctgc 2695
QY 2599 ctgttttaagcactgtgagtaaaatcttctgtcattctcaaaatatacttatata 2658
Db 2696 ctgttttaagcactgtgagtaaaatcttctgtcattctcaaaatatacttatata 2755
QY 2659 taaggaattctcacaacctaagaactagttctgcggaatgtgagcctgcgtgttaatgttcaaa 2718
Db 2756 taaggaattctcacaacctaagaactagttctgcggaatgtgagcctgcgtgttaatgttcaaa 2815
QY 2719 tcaagagcaaaagagaaatataatagtaattcttgcgttaa 2757
Db 2816 tcaagagcaaaagagaaatataatagtaattcttgcgttaa 2854
RESULT 6
X78807
ID X78807 standard; cDNA; 3093 BP.
XX
AC X78807;
XX
DT 06-SEP-1999 (first entry)
XX
DE Human nmr7 cDNA;
XX

QY 379 ccatgaaacgcaacgcccggctggaagtgcccttcggaaagggccctggagatcaacc 438
 Db 506 ccatgaaacgcaacgcccggctggaagtgcccttcggaaagggccctggagatcaacc 565
 QY 439 ggaagaaacccggcgcaagtgccagagccttcgacgaagtgctggagagcgagca 498
 Db 566 ggaagaaacccggcgcaagtgccagagccttcgacgaagtgctggagagcgagca 625
 QY 499 agaaagaaatgatcatgctccgaagagccgctggagagagagcgcccttgatcaagcgga 558
 Db 626 agaaagaaatgatcatgctccgaagagccgctggagagagagcgcccttgatcaagcgga 685
 QY 559 agaaagaaatgatcatgctccgaagagccgctggagagagagcgcccttgatcaagcgga 618
 Db 666 agaaagaaatgatcatgctccgaagagccgctggagagagagcgcccttgatcaagcgga 745
 QY 619 ggaatgatcatgcaagagagccttgagagccttcagatgaaaccccttgacataccttcacc 678
 Db 746 ggaatgatcatgcaagagagccttgagagccttcagatgaaaccccttgacataccttcacc 805
 QY 679 attcaagaattccggctgcccaggggtgcttagagagtgctgagagtgccagagctc 738
 Db 806 attcaagaattccggctgcccaggggtgcttagagagtgctgagagtgccagagctc 865
 QY 739 tgcagagcccatcgaggggaagaaagctgccaagtgagagccaggtcccgaaagatctgct 798
 Db 866 tgcagagcccatcgaggggaagaaagctgccaagtgagagccaggtcccgaaagatctgct 925
 QY 799 ctctgaagagctctctgcaagctgcccggggagagagtgagagtgctggaatacaaacccc 858
 Db 926 ctctgaagagctctctgcaagctgcccggggagagagtgagagtgctggaatacaaacccc 985
 QY 859 cagccgcaagtgagggggaagaaagatctctccctgctgcccccaatagctgtaactgtcaa 918
 Db 986 cagccgcaagtgagggggaagaaagatctctccctgctgcccccaatagctgtaactgtcaa 1045
 QY 919 cctaatgttcaaaagagcattcaagcttgcgaagtgatctctcaactcggagagctg 978
 Db 1046 cctaatgttcaaaagagcattcaagcttgcgaagtgatctctcaactcggagagctg 1105
 QY 979 ccatcgagagcagaatctcctctgctgcaagggggccgcttcgagctgctgtaactgagat 1038
 Db 1106 ccatcgagagcagaatctcctctgctgcaagggggccgcttcgagctgctgtaactgagat 1165
 QY 1039 tcaaacacgctgttcaaacgagagagctggaacctggagtgccggctgtcccaactgct 1098
 Db 1166 tcaaacacgctgttcaaacgagagagctggaacctggagtgccggctgtcccaactgct 1225
 QY 1099 tggaaagacacgagtgagcttccagcaactctcaactgagagcccatgctgtaactcaact 1158
 Db 1226 tggaaagacacgagtgagcttccagcaactctcaactgagagcccatgctgtaactcaact 1285
 QY 1159 acatgctgaaagagctgcaagctgcaagagagagagatgctgctgtaactgagagcactcc 1218
 Db 1286 acatgctgaaagagctgcaagctgcaagagagagagatgctgctgtaactgagagcactcc 1345
 QY 1219 tcttctcccccagagcccgagtgctgctgcaagacccgctgctgtaactgagagagc 1278
 Db 1346 tcttctcccccagagcccgagtgctgctgcaagacccgctgctgtaactgagagagc 1405
 QY 1279 aatcgccattactctgagagctcctcaatctgtaactgcaactcggcccgagcctgctatagct 1338
 Db 1406 aatcgccattactctgagagctcctcaatctgtaactgcaactcggcccgagcctgctatagct 1465
 QY 1339 tcttctcctgaaagatcatgctgctgcaagagctcccgagagatcaatgctcagagac 1398
 Db 1466 tcttctcctgaaagatcatgctgctgcaagagctcccgagagatcaatgctcagagac 1525
 QY 1399 cccagcgagctgctgcaatccagagacatacacccttctgtaagccctcaatgagagagct 1458
 Db 1526 cccagcgagctgctgcaatccagagacatacacccttctgtaagccctcaatgagagagct 1585

QY 1459 tcttcgcatcacaagtgatgagcgtgccccttggtggaacctccgagagcagcca 1518
 Db 1586 tcttcgcatcacaagtgatgagcgtgccccttggtggaacctccgagagcagcca 1645
 QY 1519 gaccagagaccccttgagcgcgcacactccgggccaagagatgagacatgccaagagcc 1578
 Db 1646 gaccagagaccccttgagcgcgcacactccgggccaagagatgagacatgccaagagcc 1705
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 Db 1706 gacaatgcccctgctgagcgtctccctagaggaattccctgctgtaactgagcgtgagctt 1765
 QY 1639 cctcagagagacatgagtggtcccccaccccaagctcaagctgtagagagtagagcaca 1698
 Db 1766 cctcagagagacatgagtggtcccccaccccaagctcaagctgtagagagtagagcaca 1825
 QY 1699 gactcttaagtgagagagtgacatgacatgtagagagacatcagagagagagagtgctc 1758
 Db 1826 gactcttaagtgagagagtgacatgacatgtagagagacatcagagagagagagtgctc 1885
 QY 1759 ccttccctttaaagagccctgctgctgagagagaaatccctcaagatcccaataggt 1818
 Db 1886 ccttccctttaaagagccctgctgctgagagagaaatccctcaagatcccaataggt 1945
 QY 1819 caaggtgtgagagagagcacaagcagacaaagatagagccatctgaggtctatgcccacatc 1878
 Db 1946 caaggtgtgagagagagcacaagcagacaaagatagagccatctgaggtctatgcccacatc 2005
 QY 1879 caaggtgtgagagagcctctgagagcttcttcatgctacacttaagagctcgtctccact 1938
 Db 2006 caaggtgtgagagagcctctgagagcttcttcatgctacacttaagagctcgtctccact 2065
 QY 1939 tcccactgctcccccctcctccctcagagcgtgcttgaggctcaagcctgagatcagtg 1998
 Db 2066 tcccactgctcccccctcctccctcagagcgtgcttgaggctcaagcctgagatcagtg 2125
 QY 1999 caggtgcatgagatctgtgg 2019
 Db 2126 caggtgcatgagatctgtgg 2146

RESULT 8
 X89080
 ID X89080 standard; DNA; 2068 BP.
 XX
 AC X89080;
 XX
 DT 14-SEP-1999 (first entry)
 XX
 DE Human steroid and xenobiotic receptor (SXR) encoding DNA.
 XX
 KW Nuclear receptor; SXR; steroid and xenobiotic receptor; RXR; human;
 KW retinoid X receptor; P450 gene; steroid hormone; steroid metabolism;
 KW phytoestrogen; calcium-channel blocker; steroid toxicity; tuberculosis;
 KW breast cancer; osteoporosis; Cushing syndrome; virilism; hirsutism;
 KW polycystic ovarian disease; cancer; colorectal; prostatic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS 583..1887
 FT /tag= a
 FT /transl_except= (pos:1261..1263, aa:Xaa)
 FT /note= "Xaa= unknown; the start codon is not indicated"
 PN WO9935246-A1.
 PD 15-JUL-1999.
 XX
 XX 08-JAN-1999; 99MO-0500490.
 PF 09-JAN-1998; 98US-0005286.
 XX

PA (SALK) SALK INST BIOLOGICAL STUDIES.

XX Blumberg B, Evans RM;

DR WPI: 1999-419349/35.

DR P-PSDB: Y21799.

XX New steroid and xenobiotic receptor, used to identify modulators for
PT controlling metabolism of steroids and xenobiotics, e.g. reducing
PT their toxicity

PS Claim 10: Fig 1A: 83pp: English.

CC The invention relates to a novel nuclear receptor polypeptide, designated
CC SXR (steroid and xenobiotic receptor). SXR (1) forms a heterodimer with
CC retinoid X receptor (RXR), (11) binds to a direct or inverted repeat
CC response element motif based on the half-site AGGTCA, (111) activates
CC transcription through response elements present in steroid-inducible P450
CC genes, in response to a wide variety of natural and synthetic steroid
CC hormones and (iv) is prominently expressed in liver and intestine. SXR
CC regulates expression of catabolic enzymes, in response to many different
CC steroids, and thus affects metabolism. SXR is a broad specificity, low-
CC affinity receptor for reducing excessive levels of steroids in the
CC circulation. (Antagonists of SXR are used to regulate metabolism of
CC steroids particularly phytoestrogens or calcium-channel blockers, to
CC reduce steroid toxicity in subjects being treated with steroids, e.g. in
CC cases of tuberculosis (treated with rifampin and related compounds),
CC breast cancer (treated with tamoxifen, raloxifen etc.) or osteoporosis
CC (treated with Vitamin K), or to slow metabolism of therapeutic steroids.
CC Also, modulating endogenous SXR is used to treat disease, particularly
CC an agonist is used where endogenous steroid levels are excessive (e.g.
CC Cushing syndrome; virilism and hirsutism in women; polycystic ovarian
CC disease; 11 beta-, 17- or 21-hydroxylase deficiency; 3 beta-hydroxysteroid
CC dehydrogenase deficiency, or breast, colorectal or prostatic cancer),
CC while antagonists are used where endogenous steroid levels are too low.
CC Cells that express SXR are used to identify compounds likely to be
CC involved in undesirable drug interactions. Antibodies specific for SXR
CC are used in immunohistochemical testing for studying distribution/
CC expression density of SXR, also for diagnosis and therapeutically as
CC antagonist. The present sequence represents the longest SXR cDNA clone
CC encoding the SXR polypeptide.

CC Sequence 2068 BP; 520 A; 541 C; 586 G; 420 T; 1 other;

Query Match 52.3%; Score 1466.6; DB 20; Length 2068;
Best Local Similarity 98.8%; Pred. No. 5.1e-294;
Matches 1508; Conservative 0; Mismatches 15; Indels 3; Gaps 3;

QY 139 agtggcttcaaacctccagagagccagaaagcaaacctggaggtgagaccacaaagaa 198
DB 545 actaacacacaaagagccaaagagcccaagaaacccggagggagaccccaagaa 604
QY 199 gctggaaacatgtctgacttctgacactgtgagagacacagagctgttcttgaaagcca 258
DB 605 gctggaaacatgtctgacttctgacactgtgagagacacagagctgttcttgaaagcca 664
QY 259 gcttcaacagcagatgagagagtcggaggtcccaaatcgtcgatgtggtgagaaag 318
DB 665 gcttcaacagcagatgagagagtcggaggtcccaaatcgtcgatgtggtgagaaag 724
QY 319 ccaactggtctcaactcaatgcatgcatgataagagatcaaggagcttttcaaggag 378
DB 725 ccaactggtctcaactcaatgcatgcatgataagagatcaaggagcttttcaaggag 784
QY 379 ccatgaaacacgaacgcgcgctgagtgcccttcggaaaggcgctgagagatcacc 438
DB 785 ccatgaaacacgaacgcgcgctgagtgcccttcggaaaggcgctgagagatcacc 844
QY 439 ggaagacccggcgacagtcgcaagcgcgcgctgagtgcccttcggaaaggcgctgag 498
DB 845 ggaagacccggcgacagtcgcaagcgcgcgctgagtgcccttcggaaaggcgctgag 904

QY 499 agaaagagatgatcatgtccagacagcgctgagagagagcggtcttgatcaagcgga 558
DB 905 agaaagagatgatcatgtccagacagcggtgagagagagcggtcttgatcaagcgga 964
QY 559 agaaagagatgatcatgtccagacagcggtgagagagagcggtcttgatcaagcgga 618
DB 965 agaaagagatgatcatgtccagacagcggtgagagagagcggtcttgatcaagcgga 1024
QY 619 ggaatgatgatcagagagagctgagagatgagagatgagaaacatttgacatcttccc 678
DB 1025 ggaatgatgatcagagagagctgagagatgagagatgagaaacatttgacatcttccc 1084
QY 679 attcaagaatttcctcgctgcaggggtcttagcagatgtgagatgtgcagagctc 738
DB 1085 attcaagaatttcctcgctgcaggggtcttagcagatgtgagatgtgcagagctc 1144
QY 739 tgcagagcccatcgag 798
DB 1145 tgcagagcccatcgag 1204
QY 799 ctgtgagagctctcttcgc-agctcgaggggagagagagagagagagagagagagagag 857
DB 1205 ctgtgagagctctcttcgcag 1264
QY 858 ccagcgcagctgtgag 917
DB 1265 ccagcgcagctgtgag 1323
QY 918 acctaatgttcaagagatcatcatcagcttgcagagatcttccatcttcaagagctg 977
DB 1324 acctaatgttcaagagatcatcatcagcttgcagagatcttccatcttcaagagactg 1383
QY 978 cccatgag 1037
DB 1384 cccatgag 1443
QY 1038 ttcaacacagatgttcaadgagagagagagagagagagagagagagagagagagagag 1097
DB 1444 ttcaacacagatgttcaadgagagagagagagagagagagagagagagagagagagag 1503
QY 1098 ttgagagacactgag 1157
DB 1504 ttgagagacactgag 1563
QY 1158 tacatgctgag 1217
DB 1564 tacatgctgag 1623
QY 1218 ctcttctccacagacgcgcag 1277
DB 1624 ctcttctccacagacgcgcag 1683
QY 1278 caattgcacattactctgag 1337
DB 1684 caattgcacattactctgag 1743
QY 1338 ttcttgcctcgtgag 1397
DB 1744 ttcttgcctcgtgag 1803
QY 1398 acccagcgctgtcgtgag 1457
DB 1804 acccagcgctgtcgtgag 1863
QY 1458 ttgttcgagcatcacaag 1517
DB 1864 ttgttcgagcatcacaag 1922
QY 1518 agacacag 1577
DB 1923 agacacag 1982
QY 1578 ggaacatgcccctgtgag 1637


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Oy 1440 acgccccatgcaggaggtcttgcgcatacaaggtactga 1481
    |||||
Db 1381 acgccccatgcaggaggtcttgcgcatacaaggtactga 1422
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RESULT 10

ID X59967 standard; DNA; 1374 BP.

AC X59967;

DT 04-AUG-1999 (first entry)

DE DNA encoding an intranuclear receptor protein.

Kv Human; intranuclear receptor protein; drug development; diagnosis;

treatment; ss.

05 Homo sapiens.

PN JP11127872-A.
YY

PD 18-MAY-1999
YY

PF 07-ADG-1998; 98JP-0224172.
yy

PR 11-AUG-1997; 97JP-0230335.
YY

PA (NISB) JAPAN TOBACCO INC.
YY

DR WPI; 1999-350330/30.
DR P-PSDB: Y15932

XX

DT New Intronic

PT diagnosis and treatment of disease

PS Claim 4; page 23-25; 38pp; Japanese.
XX

CC The present sequence encodes a human intranuclear receptor protein.

CC library using a welllsh ANO23 derived probe. The protein can
CC be used for the development of drugs and diagnosis and treatment

CC OF VARIOUS DISEASES.
XX

sequence 13/4 BP; 3/5 A; 3/5 C; 4/6 G; 2/6 T; 0 other;

Query Match 47 59: Score 1330 2: DB 20: Length 1374:

Best Local Similarity 99.4%; Pred. NO. 6.7e-266;
Matches 1335: Conservative 0: Mismatches 8: Indels 0:

139 attgacctcaaacatccaaagagcccaagaaacaaacctgaaagatgaa

Query Match	47.5%	Score 1330.2;	DB 20;	Length 1374;
Best Local Similarity	99.4%;	Pred. No. 6.7e-26;		
Matches 1335; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

Qy	139	agtttgcttccaaacccaacccaagagccccaagagcaaacaccttgaggttgaaagcccaaaagaa	198
Db	32	acttaaccacaagcagctccaaagagcccaagaagcaaaccttgaggttgaaagcccaaaagaa	91
Qy	199	gcttggaacacatgtgactcttgtaacatctgtgaagacacagaatctgtcttccttgaaagccca	258
Db	92	gcttggaacacatgtgactcttgtaacatctgtgaagacacagaatctgtcttccttgaaagccca	151
Qy	259	gtgtcaagcagatgaaagaaatcagaaagtccccaatctgcgctgtatgttgaggaacaag	318
Db	152	gtgtcaagcagatgaaagaaatcagaaagtccccaatctgcgctgtatgttgaggaacaag	211
Qy	319	gcacatgcgcatactaatctcaatgtccatgaaatcttgaaagatgcaaaagagcctttctcaagag	378
Db	212	gcacatgcgcatactaatctcaatgtccatgaaatcttgaaagatgcaaaagagcctttctcaagag	271
Qy	379	ccatgaaacagcaagcccgagctgaaagtgcgcccttcggaagagagcgccctgcagatccacc	438
Db	272	ccatgaaacagcaagcccgagctgaaagtgcgcccttcggaagagagcgccctgcagatccacc	331
Qy	439	ggaaagaccgagcagagtgccagagccctgcgcctgcagaaatgaccttgaaagacgagcata	498

Db	332	ggaagaaacccggcgaacaagctgacaaagccttcgcgccttcgcgaagatgcctcgaagagcgcgaatga	391
Qy	499	agaaagagaaatgatcatctctccgaacgaaagccggctgagagagaaagccgcggctctgatcaaaacgga	558
Db	392	agaaagagagaaatgatcatctctccgaacgaaagccggctgagagagaaagcgcggctctgatcaaaacgga	451
Qy	559	agaaagaaatgaaacggaacgaagagaaatcacaacaccttcgagagctgcagaagcttgaaacaaagagacagc	618
Db	452	agaaagaaatgaaacggaacgaagagaaatcacaacaccttcgagagctgcagaagcttgaaacaaagagacagc	511
Qy	619	ggaatgaatgaacaaagagagcctgaatgaagacacaaatgaataaaaccttcgtacaacacacacacacacac	678
Db	512	ggaatgaatgaacaaagagagcctgaatgaagacacaaatgaataaaaccttcgtacaacacacacacacacac	571
Qy	679	atttcacaagaattccacggcttcgcacaaagctgacttaagaatgagctgcggagtctgcacaagatctc	738
Db	572	atttcacaagaattccacggcttcgcacaaagctgacttaagaatgagctgcggagtctgcacaagatctc	631
Qy	739	tgcacagccccaatcagaaagagaaagctgcgcacaagctgaaagccaaagctccagtgaaagaaatctgagct	798
Db	632	tgcacagccccaatcagaaagagaaagctgcgcacaagctgaaagccaaagctccagtgaaagaaatctgagct	691
Qy	799	ctttgaaagagctctctctgcacagctgcggcgaggagaaatgagcagctctctgcgaacacaaacaccc	858
Db	692	ctttgaaagagctctctctgcacagctgcggcgaggagaaatgagcagctctctgcgaacacaaacaccc	751
Qy	859	cagacgaaacagtgagcggggaagaaagatctctccctcgcctgcgcacaaatggcctgaacatgctcaa	918
Db	752	cagacgaaacagtgagcggggaagaaagatctctccctcgcctgcgcacaaatggcctgaacatgctcaa	811
Qy	919	ccttcacatgcttcacaagagcacaatcaagctttgcaccaagctcatctccacattccagcgagcttgc	978
Db	812	ccttcacatgcttcacaagagcacaatcaagctttgcaccaagctcatctccacattccagcgagcttgc	871
Qy	979	ccatccagcgagccaaagatctcccttcgtaaaagggggccgccttcgaaagcttgctgcacaacgaaat	1038
Db	872	ccatccagcgagccaaagatctcccttcgtaaaagggggccgccttcgaaagcttgctgcacaacgaaat	931
Qy	1039	tcaaacacaagaatgcttcacaagcgggaagaaatctgaaagaccttgagagatgctgcgcggctgtctcatctgct	1098
Db	932	tcaaacacaagaatgcttcacaagcgggaagaaatctgaaagaccttgagagatgctgcgcggctgtctcatctgct	991
Qy	1099	tggaaagacacatgacagatgagctcttcacagcaacacctctacatgaaagcccaatgcctgaaatctcaat	1158
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Qy	1159	acaaatgcctgaagaaagccttcacagcttcgaagaaagagaaatgctgtctgaatgaaagcacaatctccc	1218
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Db	1112	tctctctccccaagaaacggccagctgctgctgcagaacacggctggctgaaacacgaatctgcgaagagac	1171
Qy	1279	aattccgcacatgaactctgaagatcctcaacattgaaatgaaatccgcgcacacgcctgcctcaatagct	1338
Db	1172	aattccgcacatgaactctgaagatcctcaacattgaaatgaaatccgcgcacacgcctgcctcaatagct	1231
Qy	1339	tcttgcttcctcgaagaaatataatgctcattgctcaacggagctccagcagacataaagtctcagacaa	1398
Db	1232	tcttgcttcctcgaagaaatataatgctcattgctcaccggagctccagcagacataaagtctcagacaa	1291
Qy	1399	ccaaagcgagctctctcgcagatccaaagaaatacaaccccttcgtacagcccccacatctgcagagagct	1458
Db	1292	ccaaagcgagctctctcgcagatccaaagaaatacaaccccttcgtacagcccccacatctgcagagagct	1351
Qy	1459	tgttcgcacatcaacagatagctga	1481
Db	1352	tgttcgcacatcaacagatagctga	1374
RESULT 11			
X59966			

RESULT	11
X59966	

ID X59966 standard; DNA: 1305 BP.
 AC X59966;
 XX 04-AUG-1999 (first entry)
 DT 04-AUG-1999 (first entry)
 DE DNA encoding an intranuclear receptor protein.
 XX Human; intranuclear receptor protein; drug development; diagnosis;
 KW treatment; ss.
 XX Homo sapiens.
 OS JP1127872-A.
 PN 18-MAY-1999.
 PD 07-AUG-1998; 98JP-0224172.
 PF 11-AUG-1997; 97JP-0230335.
 PR (NIBS) JAPAN TOBACCO INC.
 PA WPI: 1999-350330/30.
 DR P-PSDB; Y15931.
 XX New intranuclear receptor protein - useful for drug development and
 PT diagnosis and treatment of disease
 PS Claim 4; Page 22-23; 38pp; Japanese.
 XX The present sequence encodes a human intranuclear receptor protein.
 CC The nucleic acid sequence was isolated from a human adult cDNA
 CC library using a swedish ANO23 derived probe. The protein can
 CC be used for the development of drugs and diagnosis and treatment
 CC of various diseases.
 XX Sequence 1305 BP; 304 A; 356 C; 386 G; 259 T; 0 other;
 SQ

Query Match 46.6%; Score 1305; DB 20; Length 1305;
 Best Local Similarity 100.0%; Pred. No. 1.1e-260;
 Matches 1305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 ctgagggctgagagcccaagaagctggaacatgctgacttctgaactgtgagagacaca 236
 DB 1 ctgagggctgagagcccaagaagctggaacatgctgacttctgaactgtgagagacaca 60
 QY 237 gactgtctctggaagccagtgctcaacgagatgaggaagtcggaagtcgcccaatc 296
 DB 61 gactgtctctggaagccagtgctcaacgagatgaggaagtcggaagtcgcccaatc 120
 QY 297 tggcgtgctgagggagagagccacgtgctatcatcctcaatgtatgactgtgagaga 356
 DB 121 tggcgtgctgagggagagagccacgtgctatcatcctcaatgtatgactgtgagaga 180
 QY 357 tgcagagggcttttccagagagccatgaaacgcaacgcccgtgaggtgcccctccg 416
 DB 181 tgcagagggcttttccagagagccatgaaacgcaacgcccgtgaggtgcccctccg 240
 QY 417 aagggcgctcgagatcaccccggaagaccgagcagtgccagcctcgccgctcgcc 476
 DB 241 aagggcgctcgagatcaccccggaagaccgagcagtgccagcctcgccgctcgcc 300
 QY 477 aagtgctgagagagcgagatgaagaagagatgactgtccgacgagccgtgagagag 536
 DB 301 aagtgctgagagagcgagatgaagaagagatgactgtccgacgagccgtgagagag 360
 QY 537 aggcggcgcttgatcaaacggaagaaagtgaacgagacgagactcaacacactggagtg 596
 DB 361 aggcggcgcttgatcaaacggaagaaagtgaacgagacgagactcaacacactggagtg 420
 QY 597 caggggctgacagagagcagcgagatgactcaggagactgagagcgtcagatgaa 656

DB 421 caggggctgacagagagcagcgagatgactcaggagactgagagcgtcagatgaa 480
 QY 657 accttgacaatcactctccatccatgaagaattccggctgcagaggtgtgcttagcag 716
 DB 481 accttgacaatcactctccatccatgaagaattccggctgcagaggtgtgcttagcag 540
 QY 717 ggcctgaggttgcagagctctgcaaggcccatgcaagggaagaagctccaaagtgaac 776
 DB 541 ggcctgaggttgcagagctctgcaaggcccatgcaagggaagaagctccaaagtgaac 600
 QY 777 caggtcggagaagatctgtctcttgaaggtctctctgcaagctgcgggggagagatggc 836
 DB 601 caggtcggagaagatctgtctcttgaaggtctctctgcaagctgcgggggagagatggc 660
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 DB 661 agtgtctggaactacaacaccccgagcagacagtgaggcggaagaagatctctccctgctg 720
 QY 897 ccccaatgctgacatgctaacctacatgcttcaagaagcatalcagcttgcacaaagtc 956
 DB 721 ccccaatgctgacatgctaacctacatgcttcaagaagcatalcagcttgcacaaagtc 780
 QY 957 atctctactcagaggacttgcccatcgagagacacagatccctctgtaaggggccgct 1016
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 QY 1017 ttgagagtggttaactgagatcaacacagtggttcaagcgagagatggaacccggag 1076
 DB 841 ttgagagtggttaactgagatcaacacagtggttcaagcgagagatggaacccggag 900
 QY 1077 tggcgccgctgctcactcagcttggaagacacatgctgaggtgttcagaactctactg 1136
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 QY 1137 gaagccatgctgaatccaactacatgctgaagaagctgcaagtcgatgagagagatg 1196
 DB 961 gaagccatgctgaatccaactacatgctgaagaagctgcaagtcgatgagagagatg 1020
 QY 1197 gtgctgctgagagccatctccctctctccccaagaccccgagtggtgtagaacgcgc 1256
 DB 1021 gtgctgctgagagccatctccctctctccccaagaccccgagtggtgtagaacgcgc 1080
 QY 1257 gtgctgagacagctgcaagagacatcgcacatctcctaactgaactgaatgaacat 1316
 DB 1081 gtgctgagacagctgcaagagacatcgcacatctcctaactgaactgaatgaacat 1140
 QY 1317 cggcccaagctgtctatagtggttctgtctcctgaagatcaatgctatgctcaccgagctc 1376
 DB 1141 cggcccaagctgtctatagtggttctgtctcctgaagatcaatgctatgctcaccgagctc 1200
 QY 1377 cgcagatataatgctagacacaccccgagcgtgctgagcagatccagaagatatacccttt 1436
 DB 1201 cgcagatataatgctagacacaccccgagcgtgctgagcagatccagaagatatacccttt 1260
 QY 1437 gctacgcccctcatgacagagtggttcgcatcacacagtgagtga 1481
 DB 1261 gctacgcccctcatgacagagtggttcgcatcacacagtgagtga 1305

RESULT 12
 X59972
 ID X59972 standard; DNA: 644 BP.
 AC X59972;
 XX 04-AUG-1999 (first entry)
 DT 04-AUG-1999 (first entry)
 DE SEQ ID 12 of JP1127872.
 XX Human; intranuclear receptor protein; drug development; diagnosis;
 KW treatment; ss.
 XX

OS Homo sapiens.
 XX JPI127872-A.
 XX 18-MAY-1999.
 PD 07-AUG-1998; 98JP-0224172.
 XX 11-AUG-1997; 97JP-0230335.
 PR (NTSB) JAPAN TOBACCO INC.
 XX WPI: 1999-350330/30.
 DR
 XX New intranuclear receptor protein - useful for drug development and
 PT diagnosis and treatment of disease
 PT
 XX Disclosure: Page 32, 38pp; Japanese.
 PS
 XX The specification describes a human intranuclear receptor protein.
 CC The nucleic acid sequence was isolated from a human adult cDNA
 CC library using a swellfish ANO23 derived probe. The protein can
 CC be used for the development of drugs and diagnosis and treatment
 CC of various diseases. The present sequence was used in the course of
 CC the invention.
 XX
 SQ Sequence 644 BP; 175 A; 161 C; 193 G; 115 T; 0 other;

Query Match 15.2%; Score 425.2; DB 20; Length 644;
 Best Local Similarity 98.2%; Pred. No. 4.5e-79;
 Matches 430; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 139 agtggcttcaaacatccaaagagcccaagaaacatgagtgagaccacaagaa 198
 DB 138 acttaccacacagagcccaagagcccaagaaacatgagtgagaccacaagaa 257
 QY 199 gctggaacacatgctgactgtacactgtgagacacagagctgtctctggaagccca 258
 DB 258 gctggaacacatgctgactgtacactgtgagacacagagctgtctctggaagccca 317
 QY 259 gtgtcaacgcagatgagagagtcgagagtcgccaaatctgcgtgtatgtgaggaagg 318
 DB 318 gtgtcaacgcagatgagagagtcgagagtcgccaaatctgcgtgtatgtgaggaagg 377
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 QY 439 ggaagacccgcgagacagtgccagagctgcgcctgcgcaagatgacctggaagcgcatga 498
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 QY 499 aagaagagatgctatgtctcgaagggccgctggaagagagagggccttgatcaagcgga 558
 DB 558 aagaagagatgctatgtctcgaagggccgctggaagagagagggccttgatcaagcgga 617
 QY 559 aagaagatgacgagacag 576
 DB 618 aagaagatgacgagacag 635

RESULT 13
 V03129
 ID V03129 standard; CDNA; 1960 BP.
 AC V03129;
 XX 11-JUN-1998 (first entry)

XX CDNA encoding rat vitamin D receptor (VDR).
 DE
 XX Rat; vitamin D receptor; isoform protein; VDR1; VDR0; diagnosis;
 KM dominant negative receptor; signal transmission channel;
 KM bone density disorder; screening; ds.
 OS
 XX Rattus rattus.
 XX
 FH Key Location/Qualifiers
 FT CDS .12..1283
 FT /tag-
 FT /transl_except- (pos:1089..1091, aa:gly)
 W09747172-A1.
 PD 18-DEC-1997.
 XX 10-JUN-1997; 97WO-IB00947.
 PF 10-JUN-1996; 96JP-0194179.
 PR (CHUS) CHUGAI PHARM CO LTD.
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX Kato S, Ueno K;
 PI
 DR WPI: 1998-051917/05.
 DR P-PSDB; W47509.
 XX
 PT DNA encoding a vitamin D receptor isoform protein - useful for bone
 PT density determination and for screening substances for vitamin D
 PT activity
 PT
 PS Disclosure: Fig 1; 46pp; Japanese.
 XX
 CC A novel CDNA sequence encodes the rat vitamin D receptor isoform
 CC protein (VDR1). The isoform differs from the normal receptor
 CC (VDR0), which is encoded by the present sequence, in having the
 CC vitamin D response element curtailed by 86 residues, and having an
 CC extra 19 residues inserted at the C-terminal of this element. It
 CC acts as a dominant negative receptor in the vitamin D signal
 CC transmission channel.
 CC The isoform protein can be used to diagnose bone density disorders,
 CC and screen for substances having potential vitamin D-like activity.
 CC
 SQ Sequence 1960 BP; 432 A; 620 C; 497 G; 411 T; 0 other;

Query Match 10.0%; Score 278.8; DB 19; Length 1960;
 Best Local Similarity 55.6%; Pred. No. 1.1e-48;
 Matches 629; Conservative 0; Mismatches 482; Indels 21; Gaps 4;

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 DB 72 ccccgagctcgtgtgtgtgtggaacagccagcagagcttcaatcatgtcatgacc 131
 QY 348 ttgtgaagatgcaagagcttttcagagggccatgaagcacaagcccgctggaagtc 407
 DB 132 ttgtgaagatgcaagagcttttcagagggccatgaagcacaagcccgctggaagtc 191
 QY 408 cccctcggaaaggcgccctgcgagatcaaccgggaagaccggcgagatgccaagctgc 467
 DB 192 cccctc---aatgagagattccgcacatcaaccgaagaaacccggcgagatgccaagctgc 248
 QY 468 cgcctgcgaagtgctcggagagcgccatgaagagagagatgcatgtctcgaagggcc 527
 DB 249 cgggtcaaacgctgtgtggaacatcgccatgatgaagagatgcatgtctcgaagggcc 308
 QY 528 gtgagagagagggcgccctgcatcaagcggaagaaagtgaaagcgagagctccgca 587
 DB 309 gtacagcgttaaggggagatgataatgaagaaagagagagagcgcttgaaagagcagt 368

Db 629 tccctccagctctgacctgacacacccctactagacatgataacacacggtctt 688
 Qy 822 cgggggag 881
 Db 689 tcaaacctgagatcag 748
 Qy 882 atctctccctgctccacacacagatgagacatgacacacacacacacacacac 941
 Db 749 cccctccatgctgcccacacacacacacacacacacacacacacacacacacac 808
 Qy 942 agcttgcac 1001
 Db 809 gggcttgcac 868
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 Db 869 cttaagtcac 928
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 Db 989 gctgggac 1048
 Qy 1173 ctgacagctcag 1232
 Db 1049 cgaacatcag 1108
 Qy 1233 cgcacagagtgctgac 1292
 Db 1109 cgcacagagtgctgac 1168
 Qy 1293 ctgaagctcctac 1352
 Db 1169 ctgacagac 1228
 Qy 1353 atcatgctcagctcagac 1404
 Db 1229 atgac 1280
 RESULT 15
 X34789
 ID X34789 standard; DNA; 1382 BP.
 AC X34789;
 XX
 DT 06-JUL-1999 (first entry)
 DE Nucleotide sequence of human vitamin D receptor (VDR) gene transcript 9.
 XX
 KW Vitamin D receptor; VDR; hVDR; variant; isoform; SRC-1; GRIP-1; TRIPB;
 KM cofactor; human; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0916872-A1.
 XX
 PD 08-APR-1999.
 PF 29-SEP-1998: 98WO-AD00817.
 PR 29-SEP-1997: 97AU-0009500.
 XX
 PA (GARV-) GARVAN INST MEDICAL RES.
 PI Crofts LA, Elsmann JA, Hancock MS, Morrison NA;
 DR WPI: 1999-263693/22.
 DR P-PSDB: Y09036.

XX New polynucleotides which encode novel isoforms of the human vitamin
 PT D receptor or variant transcripts for hVDR
 PS
 XX Claim 4; Fig 6; 56pp; English.
 CC The invention relates to isolated polynucleotides which encode novel
 CC isoforms of the human vitamin D receptor (VDR) or variant transcripts for
 CC hVDR. The polynucleotides are useful in methods for detecting agonist and
 CC /or antagonist compound of a VDR isoform. An increase or decrease in
 CC activity of the receptor may be detected by measuring changes in
 CC interactions with known cofactors (e.g. SRC-1, GRIP-1 and TRIPB) or
 CC unknown cofactors (e.g. through use of the dual hybrid system). The
 CC polynucleotides shown in X34787, X34791 and X34792 (corresponding to
 CC hVDR exon sequences) may be useful as probes for the detection of VDR
 CC variant transcripts and for assessing cell or tissue-specific expression
 CC of variant transcripts. The present sequence represents the nucleotide
 CC sequence of hVDR gene transcript 9.
 XX
 SQ Sequence 1382 BP; 310 A; 409 C; 379 G; 284 T; 0 other;
 Query Match 9.7%; Score 272.8; DB 20; Length 1382;
 Best Local Similarity 55.1%; Pred. No. 1.7e-47;
 Matches 638; Conservative 0; Mismatches 487; Indels 33; Gaps 4;
 Qy 288 ccccaatcgcgctgagtgagagagagagagagagagagagagagagagagagagag 347
 Db 159 ccccgagctggtgggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 218
 Qy 348 tctgaagagatcag 407
 Db 219 tctgaagagatcag 278
 Qy 408 ccccttcgag 467
 Db 279 ccccttcgag 335
 Qy 468 cgcctgcgag 527
 Db 336 cgcctgcgag 395
 Qy 528 gtag 587
 Db 396 gtag 455
 Qy 588 ctggag 647
 Db 456 ctggag 512
 Qy 648 cagatgaag 707
 Db 513 cagatgaag 572
 Qy 708 ctgag 749
 Db 573 ctgag 632
 Qy 750 ctgag 809
 Db 633 ctgag 692
 Qy 810 tctctgag 869
 Db 693 tctctgag 732
 Qy 870 ggcgggag 939
 Db 753 ctgag 812
 Qy 930 aaagagac 989
 Db 813 caaagagac 872

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2001, 16:45:23 ; Search time 6591.86 Seconds
(without alignments)
2175.401 Million cell updates/sec

Title: US-09-143-828-3

Perfect score: 2802
Sequence: 1 tgaatcgtggcctctctg.....aaaaaaaaaaaaaaaaaaaaa 2802

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2802	100.0	2802	10 AF084644	AF084644 Homo sapi
2	2651.2	94.6	2905	10 AF084645	AF084645 Homo sapi
3	2591.2	92.5	4448	52 HSAJ9936	AJ009936 Homo sapi
4	2359.2	84.2	4337	52 HSAJ9937	AJ009937 Homo sapi
5	1866.6	66.6	2146	10 AF061056	AF061056 Homo sapi
6	1398.8	49.9	160185	69 AC069444	AC069444 Homo sapi
7	1046	37.3	1895	3 AF182217	AF182217 Oryctolagus
8	991.4	35.4	1601	3 AF188476	AF188476 Oryctolagus
9	974.2	34.8	1709	11 AF031814	AF031814 Mus muscu
10	967.8	34.5	1755	11 AF151377	AF151377 Rattus no
11	335	12.0	365	77 G36929	G36929 SHGC-56597
12	284	10.1	1340	4 AF276753	AF276753 Gallus ga
13	280.8	10.0	1377	11 D31969	D31969 Mouse mRNA
14	278.8	10.0	2043	11 RATDHRD3	J04147 Rat 1.25-cl
15	275	9.8	2494	4 AF011356	AF011356 Gallus ga
16	272.8	9.7	1284	10 AF026260	AF026260 Homo sapi
17	272.8	9.7	1335	53 HSDVDR	X67482 H. sapiens m
18	272.8	9.7	4604	85 HSDVDR	J03258 Human vitam
19	267.8	9.6	1724	4 C7012641	U12641 Cocurnix ja
20	258.6	9.2	1638	4 XLRNAONST	X75163 X. laevis MR
21	239.8	8.6	2429	4 AB037674	AB037674 Paratrich

ALIGNMENTS

[illegible]

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 Db 2701 CCTGT 2760
 Qy 2761 aa 2802
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 LOCUS AF084645 Homo sapiens orphan nuclear receptor (PARI) mRNA, complete cds.
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 KEYWORDS
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 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 2905)
 AUTHORS
 Bertilsson, G., Heidrich, J., Svensson, K., Asman, M., Jendeborg, L.,
 Sydow-Backman, M., Ohlsson, R., Postlund, H., Blomquist, P. and
 Berkenstam, A.
 IDENTIFICATION OF A HUMAN NUCLEAR RECEPTOR DEFINES A NEW SIGNALING
 PATHWAY FOR CYP3A INDUCTION
 Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12208-12213 (1998)
 JOURNAL MEDLINE
 98445550

REFERENCE 2 (bases 1 to 2905)
 AUTHORS Bertilsson, G., Asman, M., Blomquist, P. and Berkenstam, A.
 TITLE Direct Submission
 JOURNAL Submitted (19-AUG-1998) Cell and Molecular Biology, Medical Nobel Institute, Karolinska Institute, Doktorsringen 2, Stockholm 17177, Sweden

FEATURES

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CDS

BASE COUNT 765 a 727 c 778 g 635 t
 ORIGIN

Query Match 94.68; Score 2651.2; DB 10; Length 2905;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2656; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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RESULT 3
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 LOCUS HSAJ9936 4448 bp mRNA PRI 08-SEP-1999

DEFINITION Homo sapiens mRNA for nuclear hormone receptor PRR1.
 ACCESSION AJ009936
 VERSION AJ009936.1 GI:5852062
 KEYWORDS nuclear hormone receptor; orphan nuclear receptor; PRR1 gene.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 4448)
 AUTHORS Heard, D.J., Holloway, J., Hansen, C., Tommerup, N., Aagaard, L. and Vissing, H.
 TITLE Identification of a novel protein isoform of the human nuclear hormone receptor PXR/SXR and localization to chromosome 3q12.1-13.3
 JOURNAL Eur. J. Hum. Genet. In press
 REFERENCE 2 (bases 1 to 4448)
 AUTHORS Heard, D.J.
 TITLE Direct Submission
 JOURNAL Submitted (31-JUL-1998) Heard D.J., Novo Nordisk A/S, Molecular Genetics, Novo Alle, DK-2880, Bagsvaerd, DENMARK
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CDS

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BASE COUNT 1157 a 1132 c 1095 g 1064 t
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Query Match 92.5%; Score 2591.2; DB 52; Length 4448;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 2632; Conservative 0; Mismatches 13; Indels 3; Gaps 3;

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DEFINITION	Homo sapiens orphan nuclear receptor PKR mRNA, complete cds.		
ACCESSION	AF061056		
VERSION	AF061056.1 GI:3511137		
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 2146)		
AUTHORS	Lehmann, J.M., McKee, D.D., Watson, M.A., Willson, T.M., Moore, J.T. and Kilewer, S.A.		
TITLE	The human orphan nuclear receptor PKR is activated by compounds that regulate CYP3A4 gene expression and cause drug interactions		
JOURNAL	J. Clin. Invest. 102 (5), 1016-1023 (1998)		
MEDLINE	98395173		
REFERENCE	2 (bases 1 to 2146)		
AUTHORS	Lehmann, J.M., McKee, D.D., Watson, M.A., Willson, T.M., Moore, J.T. and Kilewer, S.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-Apr-1998) Molecular Endocrinology, Glaxo Wellcome, 5		
FEATURES	Moore Drive, RTP, NC 27709, USA		
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QY 319 ccaatggtctactctcaactgatlcatgaaatgtgaagaaatgacaagggtctttcaaggagg	378				
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 Rattus.
 1 (bases 1 to 1755)
 Zhang, H., Leculysse, E., Liu, L., Hu, M., Matoney, L., Zhu, W. and Yan, B.
 Rat Pregnane X Receptor: Molecular Cloning, Tissue Distribution,
 and Xenobiotic Regulation
 Archive of Biochemistry and Biophysics 368 (1), 14-22 (1999)
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 2 (bases 1 to 1755)
 Zhang, H., Leculysse, E., Liu, L., Hu, M., Matoney, L., Zhu, W. and Yan, B.
 Direct Substitution
 Submitted (13-MAY-1999) Biomedical Sciences, University of Rhode
 Island, 41 Lower College Road, Kingston, RI 02881, USA
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DEFINITION SHGC-56397 Human Homo sapiens STS CDNA, sequence tagged site.
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VERSION G36929.1 GI:2734596
KEYWORDS STS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 365)
AUTHORS Myers,R.M.
TITLE Human STS (1997)
JOURNAL Unpublished (1997)
COMMENT

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Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: CCCATCAGTGGCAACAGCA
Primer B: AGTGAAGTTCCTCCGAGGACA
STS size: 107
PCR Profile:

Initial incubation: 95 degrees C for 10 minutes
Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 30 seconds
Polymerization: 72 degrees C for 23 seconds
PCR Cycles: 30

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Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Amplify: Gold Polymerase: 0.07 units/uL
Total Vol: 5 uL
Buffer:
-MgCl2: 2.5 mM
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-Tris-HCl: 10 mM
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Prepared with primer pairs derived from N69311 -- Unigene.
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ACCESSION AF276753
VERSION AF276753.1 GI:10505178
KEYWORDS
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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 REFERENCE 1 (bases 1 to 2494)
 Lu, Z., Hanson, K., and DeLuca, H.F.
 Cloning and origin of the two forms of chicken vitamin D receptor
 Arch. Biochem. Biophys. 339 (1), 99-106 (1997)
 MEDLINE 97223369
 JOHNNAL 2 (bases 1 to 2494)
 Lu, Z., Hanson, K., and DeLuca, H.F.
 Direct Submission
 Submitted (30-JUN-1997) Biochemistry, University of
 Wisconsin-Madison, 420 Henry Mall, Madison, WI 53706, USA
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Db 835 AACATCGAGCTGCCCCACCTCCCATGCTCCCGACCTGCGGACCTGCTGCTGCTGCTGCTGCT 894
Qy 927 ttcaagagcatcatcagcttgcgaagatcatctcactcactcactcactcactcactcag 986
Db 895 ATACAGAAAGATGATGCGCTTGCCCAAGATGATCCCGGATTCAGGAGATCTGACGGCAGAG 954
Qy 987 gacagatctccctgcctgcagagggcgcccttcgagctgctcactcactcactcactcactc 1046
Db 955 GATCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
Qy 1047 gtgttcaacgagagacggaactcggaggtg-----tgccgctgtctcactcgc 1097
Db 1015 TCCCTTACACATGAGAGACATGCTCTGAGACTGCGGAAACAAATGACTTCAAGTACAAAGTC 1074
Qy 1098 ttggaagacactgcagtgctgtcctcagcaacttctcactcactcactcactcactcactc 1157
Db 1075 AGCGATGTCACCAAGCGGAGACAGACATGAGACTCTGAGAGCGGCTGCTGAGTTCAG 1134
Qy 1158 taatgctgaagagctgcagctgcagtgagagagatgctgctgctgctgctgctgctgct 1217
Db 1135 GTGGGCTTAAAGAACTGAACCTTACGAGAAAGAGCACTGCTGCTGCTGCTGCTGCTGCTGCT 1194
Qy 1218 ctctctctcccgagccgaggtgtgtgcagcagcggtgtgtgacacagctgcagagag 1277
Db 1195 ATCTGTCCTCCAGATCGGCGCGCTGAGAGACCTCTCTGCTGAGTTCATTCAGAGAGC 1254
Qy 1278 caattcgcaattactcctgaagctcactcactcactcactcactcactcactcactcactc 1337
Db 1255 CGGCTCTGAGACATCTCCAGAGACTTACATCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1314
Qy 1338 ttctgtctcctgaagatcatgctgctcagcagctcgcagcagcagcagcagcagcagcagc 1397
Db 1315 CTGCTGTAGCGCAAGATGATCCAGAGAGCTGCGGAGCTGCGAGCCTCAAGAGAGAGCAGC 1374

Qy 1398 acccaagcgctgctgcagatccagagacatacaccccttgcctacgcccctcatgcaaggag 1457
Db 1375 TCCAAAGATTAACGGCTGCTCTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1434
Qy 1458 ttgttcgcatcagagtagc 1478
Db 1435 GTGCTGAGAGTCTGCGCAAC 1455

Search completed: February 18, 2001, 16:48:29
Job time: 11089 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 18, 2001, 13:05:04 ; Search time: 67.2 seconds

(without alignments)
824.990 Million cell updates/sec

Title: us-09-143-828-4

Perfect score: 2494
Sequence: 1 MTVTHTHHEKESGLRAPALP.....QDIHPFATPLMDELFGITGS 473

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_protent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2494	100.0	473	4	Q9UNW4
2	2330	93.4	457	4	Q9UJ26
3	2278	91.3	434	4	Q9UJ27
4	2110.5	84.6	420	4	Q9UJ23
5	2058.5	82.5	397	4	Q9UJ24
6	1973	79.1	379	4	Q9UJ25
7	1814.5	72.8	411	6	Q9UJ02
8	1753.5	70.6	432	11	Q9UJ17
9	1753.5	70.3	386	13	Q9UJ22
10	991.5	39.8	420	13	Q9UJ23
11	817	32.8	420	13	Q9UJ24
12	796	31.9	453	13	Q9UJ25
13	790.5	31.7	425	13	Q9UJ26
14	729	29.2	358	11	Q9UJ27
15	504.5	20.2	445	11	Q9UJ28
16	500.5	20.1	455	4	Q9UJ29
17	472.5	18.9	472	4	Q9UJ30
18	463	18.6	469	5	Q9UJ31
19	460	18.4	680	5	Q9UJ32

20	459	18.4	397	5	Q76246	Q76246 uca pugliat
21	457	18.3	386	13	Q9UJ26	Q9UJ26 brachydanio
22	453	18.2	673	5	Q76827	Q76827 ceratilis c
23	452.5	18.1	484	11	Q60641	Q60641 mus musculu
24	450	18.0	416	13	Q9UJ24	Q9UJ24 hipoglossu
25	447.5	17.9	456	4	Q13986	Q13986 homo sapien
26	446	17.9	454	13	Q9UJ24	Q9UJ24 fugu rubrip
27	445	17.8	541	5	Q9UJ23	Q9UJ23 fugu rubrip
28	444	17.8	447	13	Q9UJ23	Q9UJ23 fugu rubrip
29	437	17.5	881	5	Q9UJ23	Q9UJ23 fugu rubrip
30	433.5	17.4	457	13	Q9UJ23	Q9UJ23 fugu rubrip
31	432	17.3	444	13	Q9UJ23	Q9UJ23 fugu rubrip
32	431	17.3	491	5	Q9UJ23	Q9UJ23 fugu rubrip
33	428	17.2	454	13	Q9UJ23	Q9UJ23 fugu rubrip
34	425	17.0	455	13	Q9UJ23	Q9UJ23 fugu rubrip
35	424	17.0	452	13	Q9UJ23	Q9UJ23 fugu rubrip
36	424	17.0	459	11	Q9UJ23	Q9UJ23 fugu rubrip
37	422	16.9	416	13	Q9UJ23	Q9UJ23 fugu rubrip
38	422	16.9	448	13	Q9UJ23	Q9UJ23 fugu rubrip
39	421.5	16.9	401	13	Q9UJ23	Q9UJ23 fugu rubrip
40	418	16.8	410	6	Q9UJ23	Q9UJ23 fugu rubrip
41	418	16.8	453	13	Q9UJ23	Q9UJ23 fugu rubrip
42	416.5	16.7	416	4	Q9UJ23	Q9UJ23 fugu rubrip
43	416	16.7	450	18	Q9UJ23	Q9UJ23 fugu rubrip
44	416	16.7	452	11	Q9UJ23	Q9UJ23 fugu rubrip
45	416	16.7	549	13	Q9UJ23	Q9UJ23 fugu rubrip

ALIGNMENTS

RESULT	1	PRELIMINARY	PRT	473 AA
ID	Q9UNW4			
AC	Q9UNW4			
DT	01-MAY-2000 (TREMURFEL_13, Created)			
DT	01-MAY-2000 (TREMURFEL_13, Last sequence update)			
DT	01-OCT-2000 (TREMURFEL_15, Last annotation update)			
DE	ORPHAN NUCLEAR RECEPTOR.			
GN	PAR2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER.			
RX	MEDLINE=8445350; PubMed=9770465;			
RA	Bertilsson G., Heidrich J., Svensson K., Asman M., Jendeberg L.,			
RA	Sydow-Backman M., Ohlsson R., Postlund H., Blomquist P.,			
RA	Berkestan A.;			
RT	"Identification of a human nuclear receptor defines a new signaling			
RT	pathway for CYP3A induction."			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:12208-12213(1998).			
DR	EMBL; AF084644; AAC6457.1; -.			
DR	HSSP; P10826; IHRA.			
DR	INTERPRO; IPR000324; -.			
DR	INTERPRO; IPR000536; -.			
DR	INTERPRO; IPR001628; -.			
DR	INTERPRO; IPR001723; -.			
DR	PFAM; PF00104; hormone_rec; 1.			
DR	PRINTS; PF00047; STEROIDFINGER.			
DR	PRINTS; PRO0350; VITAMINR.			
DR	PRINTS; PRO0398; STRDHOMONER.			
DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.			
RW	Receptor.			
SO	SEQUENCE			

Query Match: 100.0%; Score 2494; DB 4; Length 473;
Best Local Similarity: 100.0%; Pred. NO. 3.7e-204;
Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVTTHHKEGSLRAPALPLHSAAEALASNPGRPEANLEVRPKESWNHADVHCEDTE 60
 DB 1 MTVTTHHKEGSLRAPALPLHSAAEALASNPGRPEANLEVRPKESWNHADVHCEDTE 60
 QY 61 SVPGKPSVNADEEVGGPOICRVCGKATGYHENVMTSCGCGFFRRAMKRNARLCPERRK 120
 DB 61 SVPGKPSVNADEEVGGPOICRVCGKATGYHENVMTSCGCGFFRRAMKRNARLCPERRK 120
 QY 121 GACETTRKTRROCOARLRCLESCKEMKEMTSDEAVERRALIRKKSERTGTQPLGVQ 180
 DB 121 GACETTRKTRROCOARLRCLESCKEMKEMTSDEAVERRALIRKKSERTGTQPLGVQ 180
 QY 181 GLTEQRMIRRELMADQAKTEPDTTSHFKNFRLPGVLSGCELPESLQAPREBAKMSQ 240
 DB 181 GLTEQRMIRRELMADQAKTEPDTTSHFKNFRLPGVLSGCELPESLQAPREBAKMSQ 240
 QY 241 VRKDLCSLKVSLQNGEDGSVWNYKPPADSGKEIFSLPHMADSTYMFKGIIISFAKYI 300
 DB 241 VRKDLCSLKVSLQNGEDGSVWNYKPPADSGKEIFSLPHMADSTYMFKGIIISFAKYI 300
 QY 301 SEFRDLPIEDQISLKGAFELCOLRENTVFNAETGTECGRLSTCLEDTAGGFOQLLE 360
 DB 301 SEFRDLPIEDQISLKGAFELCOLRENTVFNAETGTECGRLSTCLEDTAGGFOQLLE 360
 QY 361 PMLKHYMLKKLQHEEYVLMQATSLFSPDPGVLQHRVVDQLOEOPATILKSYIECNR 420
 DB 361 PMLKHYMLKKLQHEEYVLMQATSLFSPDPGVLQHRVVDQLOEOPATILKSYIECNR 420
 QY 421 POPARFELFKTAMLTSLRSINAOHTORLRIODIHFPATPLMOELFGITGS 473
 DB 421 POPARFELFKTAMLTSLRSINAOHTORLRIODIHFPATPLMOELFGITGS 473
 RESULT 2
 Q9UJ26 PRELIMINARY; PRT: 457 AA.
 ID Q9UJ26
 AC Q9UJ26;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE NUCLEAR HORMONE RECEPTOR PRRI-C.
 GN PRRI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard L.,
 RA Vissing H.;
 RT "Identification of a novel protein isoform of the human nuclear
 RT hormone receptor PXR/SXR and localization to chromosome 3q12.1
 RT -13.3."
 RL Eur. J. Hum. Genet. 0:0-0(0).
 DR EMBL: AJ009336; CAB55490.1;
 DR HSSP: P10826; IHRA.
 DR INTERPRO: IPR000324;
 DR INTERPRO: IPR000536;
 DR INTERPRO: IPR001628;
 DR INTERPRO: IPR001723;
 DR PFAM: PF00104; hormone_rec. 1.
 DR PFAM: PF00105; zf-C4; 1.
 DR PRINTS: PRO0047; STROIDEFINGER.
 DR PRINTS: PRO0350; VITAMINDR.
 DR PRINTS: PRO0398; STRDHOMONER.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 KW Receptor.
 SQ SEQUENCE 457 AA; 52145 MW; 812F8B354B5B784E CRC64;

Query Match 93.4%; Score 2330; DB 4; Length 457;

Best Local Similarity 98.4%; Pred. No. 3.2e-190;
Matches 442; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 25 AAEIASHPGPPANLEVRPKESWNHADVHCEDTESVGRKSVNADEEVGGPOICRVCG 84
 DB 9 AKMLPPSPGRPEANLEVRPKESWNHADVHCEDTESVGRKSVNADEEVGGPOICRVCG 68
 QY 85 DKATGYHENVMTSCGCGFFRRAMKRNARLCPERRKACETIRKTRROCOARLRCLES 144
 DB 69 DKATGYHENVMTSCGCGFFRRAMKRNARLCPERRKACETIRKTRROCOARLRCLES 129
 QY 145 GMRKEMIMSDAVERRALIRKKSERTGTQPLGVQGLTEQRMIRRELMADQAKTEPDTT 204
 DB 129 GMRKEMIMSDAVERRALIRKKSERTGTQPLGVQGLTEQRMIRRELMADQAKTEPDTT 188
 QY 205 FSHFKNFRPLPGVLSGCELPESLQAPREBAKMSQVRKDLCSLKVSLQNGEDGSVWNY 264
 DB 189 FSHFKNFRPLPGVLSGCELPESLQAPREBAKMSQVRKDLCSLKVSLQNGEDGSVWNY 248
 QY 265 KPPADSGKEIFSLPHMADSTYMFKGIIISFAKYISFRDLPIEDQISLKGAFELCO 324
 DB 249 KPPADSGKEIFSLPHMADSTYMFKGIIISFAKYISFRDLPIEDQISLKGAFELCO 308
 QY 325 LRNTVFNAETGTECGRLSTCLEDTAGGFOQLLEPMLKHYMLKKLQHEEYVLMQ 384
 DB 309 LRNTVFNAETGTECGRLSTCLEDTAGGFOQLLEPMLKHYMLKKLQHEEYVLMQ 368
 QY 385 ISLFSFDRGVLOHRVVDQLOEOPATILKSYIECNRPOPANRFLFKTAMLTSLRSINA 444
 DB 369 ISLFSFDRGVLOHRVVDQLOEOPATILKSYIECNRPOPANRFLFKTAMLTSLRSINA 428
 QY 445 QHTORLRIODIHFPATPLMOELFGITGS 473
 DB 429 QHTORLRIODIHFPATPLMOELFGITGS 457

RESULT 3
 Q9UJ27 PRELIMINARY; PRT: 434 AA.
 ID Q9UJ27
 AC Q9UJ27;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE NUCLEAR HORMONE RECEPTOR PRRI-A.
 GN PRRI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard L.,
 RA Vissing H.;
 RT "Identification of a novel protein isoform of the human nuclear
 RT hormone receptor PXR/SXR and localization to chromosome 3q12.1
 RT -13.3."
 RL Eur. J. Hum. Genet. 0:0-0(0).
 DR EMBL: AJ009336; CAB55489.1;
 DR HSSP: P10826; IHRA.
 DR INTERPRO: IPR000324;
 DR INTERPRO: IPR000536;
 DR INTERPRO: IPR001628;
 DR INTERPRO: IPR001723;
 DR PFAM: PF00104; hormone_rec. 1.
 DR PFAM: PF00105; zf-C4; 1.
 DR PRINTS: PRO0047; STROIDEFINGER.
 DR PRINTS: PRO0350; VITAMINDR.
 DR PRINTS: PRO0398; STRDHOMONER.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 KW Receptor.
 SQ SEQUENCE 434 AA; 49777 MW; AB36DEC23C4C4200 CRC64;

Query Match	91.38;	Score 2278;	DB 4;	Length 434;
Best Local Similarity	99.38;	Pred. No. 8.1e-186;		
Matches 431; conservative	1;	Mismatches 2;	Indels 0;	Gaps 0

DR PRINTS: PRO0047; STROIDFINGER.
 DR PRINTS: PRO0350; VITAMINR.
 DR PRINTS: PRO0398; STRDHOMONER.
 DR PRINTS: PRO0546; THYROIDHORM.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 DR RECEPTOR.
 KW RECEPTOR.
 SO SEQUENCE 397 AA; 45782 MW; 5E2CE0BB10663073 CRC64;

Query Match 82.5%; Score 2058.5; DB 4; Length 397;
 Best Local Similarity 90.8%; Pred. No. 3,5e-167;
 Matches 394; Conservative 1; Mismatches 2; Indels 37; Gaps 1;

QY 40 LEVAPKESWNTADYVHCEDESVPKPSVNADEEVGPQICRYCGDKATGYHFNVMTCG 99
 :|||||
 DB 1 MEVAPKESWNTADYVHCEDESVPKPSVNADEEVGPQICRYCGDKATGYHFNVMTCG 60
 QY 100 CKGFFRRAMKRNALRCPFRKACETRTKTRQCCACRLKCKESGKMKEMSDAEVEE 159
 :|||||
 DB 61 CKGFFRRAMKRNALRCPFRKACETRTKTRQCCACRLKCKESGKMKEMSDAEVEE 120
 QY 160 RRALKKRSRTGTOPGLVQGLTEEOBMIRLMDAOMKTPDTTSHKFNRLPGVLS 219
 :|||||
 DB 121 RRALKKRSRTGTOPGLVQGLTEEOBMIRLMDAOMKTPDTTSHKFNRLPGVLS 173
 QY 220 GCELPESLQAPSRBEAAKMSQVRKDCSLKVSQLRGEGDSVWNYKPPADSGKEIFSL 279
 :|||||
 DB 174 -----VSQLRGEGDSVWNYKPPADSGKEIFSL 203
 QY 280 PHNADSTYFKGIISPAKYSTFRDLPIDQISLKGAPFELCOLRFTVNAETGWE 339
 :|||||
 DB 204 PHNADSTYFKGIISPAKYSTFRDLPIDQISLKGAPFELCOLRFTVNAETGWE 263
 QY 340 CGRLSTYCEPAGFQOLLEPMKRFHYMLKQLHBEVYVLMQALSLESPDRPGVLR 399
 :|||||
 DB 264 CGRLSTYCEPAGFQOLLEPMKRFHYMLKQLHBEVYVLMQALSLESPDRPGVLR 333
 QY 400 VVDQLOQOFATILKSYIECNRPQAHNFELFKIMAMTELRSINAOHTQRLRIQ 459
 :|||||
 DB 324 VVDQLOQOFATILKSYIECNRPQAHNFELFKIMAMTELRSINAOHTQRLRIQ 383
 QY 460 ATPMOELFEGITGS 473
 :|||||
 DB 384 ATPMOELFEGITGS 397

RESULT 6
 ID 09U025 PRELIMINARY; PRT; 379 AA.

AC 09U025;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE NUCLEAR HORMONE RECEPTOR PRAL-B.
 GN PRAL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard L.,
 RA Vissing H.;
 RT "Identification of a novel protein isoform of the human nuclear
 RT hormone receptor PXR/SXR and localization to chromosome 3q12.1
 RT -13.3.";
 RL Eur. J. Hum. Genet. 0:0-0(0).
 DR EMBL: AJ009936; CAB5491.1; -.
 DR HSSP: P10826; 1HRA.
 DR INTERPRO: IPR000324; -.
 DR INTERPRO: IPR000536; -.
 DR INTERPRO: IPR001628; -.

DR INTERPRO: IPR001723; -.
 DR PFAM: PF00104; hormone_rec. 1.
 DR PFAM: PF00105; zf-CA. 1.
 DR PRINTS: PRO0047; STROIDFINGER.
 DR PRINTS: PRO0350; VITAMINR.
 DR PRINTS: PRO0398; STRDHOMONER.
 DR RECEPTOR.
 KW RECEPTOR.
 SO SEQUENCE 379 AA; 43692 MW; 8F7B7AFA13E45036 CRC64;

Query Match 79.1%; Score 1973; DB 4; Length 379;
 Best Local Similarity 99.7%; Pred. No. 6.2e-160;
 Matches 378; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 95 MTCEGCKGFFRRAMKRNALRCPFRKACETRTKTRQCCACRLKCKESGKMKEMSD 154
 :|||||
 DB 1 MTCEGCKGFFRRAMKRNALRCPFRKACETRTKTRQCCACRLKCKESGKMKEMSD 60
 QY 155 EAVEERALLIKRKSERTGTOPGLVQGLTEEOBMIRLMDAOMKTPDTTSHKFNRLP 214
 :|||||
 DB 61 EAVEERALLIKRKSERTGTOPGLVQGLTEEOBMIRLMDAOMKTPDTTSHKFNRLP 120
 QY 215 GYLSSGCELPESLQAPSRBEAAKMSQVRKDCSLKVSQLRGEGDSVWNYKPPADSGKE 274
 :|||||
 DB 121 GYLSSGCELPESLQAPSRBEAAKMSQVRKDCSLKVSQLRGEGDSVWNYKPPADSGKE 180
 QY 275 IFSILPHNADSTYFKGIISPAKYSTFRDLPIDQISLKGAPFELCOLRFTVNAE 334
 :|||||
 DB 181 IFSILPHNADSTYFKGIISPAKYSTFRDLPIDQISLKGAPFELCOLRFTVNAE 240
 QY 335 TGTEWCGRLSTYCEPAGFQOLLEPMKRFHYMLKQLHBEVYVLMQALSLESPDRPG 394
 :|||||
 DB 241 TGTEWCGRLSTYCEPAGFQOLLEPMKRFHYMLKQLHBEVYVLMQALSLESPDRPG 300
 QY 395 VLOHNVVDQLOQOFATILKSYIECNRPQAHNFELFKIMAMTELRSINAOHTQRLRIQ 454
 :|||||
 DB 301 VLOHNVVDQLOQOFATILKSYIECNRPQAHNFELFKIMAMTELRSINAOHTQRLRIQ 360
 QY 455 DIHPATPMLQELFEGITGS 473
 :|||||
 DB 361 DIHPATPMLQELFEGITGS 379

RESULT 7
 ID 09U002 PRELIMINARY; PRT; 411 AA.

AC 09U002;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE PREGNANE X RECEPTOR.
 GN NR112 OR PXR.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRED NEW ZEALAND WHITE RABBIT; TISSUE=KIDNEY;
 RA Savas U., Wester M.R., Griffin K.J., Johnson E.F.;
 RT "The rabbit pregnane x receptor is activated by rifampicin";
 RT submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-20092326; PubMed-10628745;
 RA Jones S.A., Moore L.B., Shenk J.L., Wisely G.B., Hamilton G.A.,
 RA McKee D.D., Tomkinson N.C., LeCluyse E.L., Lambert M.H., Willson T.M.,
 RA Klierer S.A., Moore J.T.;
 RT "The pregnane x receptor: a promiscuous xenobiotic receptor that has
 RT diverged during evolution";
 RL Mol. Endocrinol. 14:27-39(2000).
 DR EMBL: AF182217; AAD54426.1; -.
 DR EMBL: AF188476; AAF31165.1; -.

DR INTERPRO: IPR001628; -
 DR INTERPRO: IPR001723; -
 DR INTERPRO: IPR001728; -
 DR PFAM: PF00104; hormone_rec; 1.
 DR PFAM: PF00105; zf-C4; 1.
 DR PRINTS: PR00047; STEROIDFINGER.
 DR PRINTS: PR00350; VITAMINDR.
 DR PRINTS: PR00398; STDRHOMOR.
 DR PRINTS: PR00546; THYROIDHOMR.
 DR RECEPTOR.
 KM SEQUENCE 342 AA; 39696 MW; 7C9467C3E9000A3A CRC64;
 SQ

Query Match 70.3%; Score 1753.5; DB 4; Length 342;
 Best Local Similarity 90.0%; Pred. No. 2,6e-141;
 Matches 341; Conservative 0; Mismatches 1; Indels 37; Gaps 1;

QY 95 MTCEGCKGFFRRAMRNRLRCFPRKACETTRKTRROCOACRLKCEGSKKEMIMSD 154
 |||||
 DB 1 MTCEGCKGFFRRAMRNRLRCFPRKACETTRKTRROCOACRLKCEGSKKEMIMSD 60
 QY 155 EAVEERRALIKRKSEKERTGTPGVQGLTEQRMIMRELMDAQMTFTTSHKNEFLP 214
 |||||
 DB 61 EAVEERRALIKRKSEKERTGTPGVQGLTEQRMIMRELMDAQMTFTTSHKNEFLP 118
 QY 215 GVLSSGCELPESLQAPSRSEAKNSQVAKDCLSKVSLQINGEGSSVNNYKPPADSGKE 274
 |||||
 DB 119 -----VSLQLEGGEDSSVNNYKPPADSGKE 143
 QY 275 IFSLLPHMADMTYMEKGLISPAKISYFRDLPIEDQISLKGAFELCOLRENTVNAE 334
 |||||
 DB 144 IFSLLPHMADMTYMEKGLISPAKISYFRDLPIEDQISLKGAFELCOLRENTVNAE 203
 QY 335 TGTWEGRLSYCLEDTAGGFOQLLEPMKTHYMLKQLHREEVYLMQALISLSPDRG 394
 |||||
 DB 204 TGTWEGRLSYCLEDTAGGFOQLLEPMKTHYMLKQLHREEVYLMQALISLSPDRG 263
 QY 395 VLOHNVQLOBOFAITLKSYTECHNRPOPAHREFLKIMAMTELKRSINAOTQRLRIQ 454
 |||||
 DB 264 VLOHNVQLOBOFAITLKSYTECHNRPOPAHREFLKIMAMTELKRSINAOTQRLRIQ 323
 QY 455 DIHPFATPLMOELFGITGS 473
 |||||
 DB 324 DIHPFATPLMOELFGITGS 342

RESULT 10
 Q91839 PRELIMINARY: PRT; 386 AA.
 ID 091839
 AC 091839
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ORPHAN NUCLEAR RECEPTOR OF STEROID/THYROID SUPERFAMILY.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94173664; PubMed=8127656;
 RA Smith D.P., Mason C.S., Jones E.A., Old R.W.;
 RT "A novel nuclear receptor superfamily member in Xenopus that
 associates with RXR, and shares extensive sequence similarity to the
 mammalian vitamin D3 receptor.";
 RL Nucleic Acids Res. 22:66-71(1994).
 DR EMBL; X75163; CA53006.1; -
 DR HSSP; P10826; IIRA.
 DR INTERPRO: IPR000536; -
 DR PFAM: PF00104; hormone_rec; 1.
 DR PFAM: PF00105; zf-C4; 1.

DR PRINTS: PR00047; STEROIDFINGER.
 DR PROSITE: PS00031; NUCLEAR RECEPTOR; UNKNOWN 1.
 SQ SEQUENCE 386 AA; 44302 MW; 8B046ED219556573 CRC64;

Query Match 39.8%; Score 991.5; DB 13; Length 386;
 Best Local Similarity 49.0%; Pred. No. 2,3e-76;
 Matches 204; Conservative 59; Mismatches 104; Indels 49; Gaps 9;

QY 57 EDTESVPGKPSVNADEEVGPOICRVGDKATGYHNVMTGCGCGFFRRAMRNRLRC 116
 |||||
 DB 14 EEEEDASNSCGTEDEDDDPKICRACGDRATGYHNVMTGCGCGFFRRAMRNRLRC 73
 QY 117 PFRKACETTRKTRROCOACRLKCEGSKKEMIMSDAEVARRALIKRK-KSRTGQ 175
 |||||
 DB 74 PFRKACETTRKTRROCOACRLKCEGSKKEMIMSDAEVARRALIKRK-KSRTGQ 132
 QY 176 PLGVQGLTEQRMIMRELMDAQMTFTTSHKNEFLPGVLSGCELPESLQAPSRSEA 235
 |||||
 DB 133 PLGVQGLTEQRMIMRELMDAQMTFTTSHKNEFLPGVLSGCELPESLQAPSRSEA 171
 QY 236 AKMSQVAKDCLSKVSLQINGEGSSVNNYKPPADSGKEIFSLLPHMADMTYMEKGLIS 295
 |||||
 DB 172 -----RSSDPT--OEPOATS--SEAFMLPLHISDLVTYMKGLIS 207
 QY 296 FAVIVSYFRDLPIEDQISLKGAFELCOLRENTVNAETGTEGRLSYCLEDT-AGGE 354
 |||||
 DB 208 FAVIVSYFRDLPIEDQISLKGAFELCOLRENTVNAETGTEGRLSYCLEDT-AGGE 267
 QY 355 QQLLEPMKTHYMLKQLHREEVYLMQALISLSPDRGVLOHNVQLOBOFAITLKS 414
 |||||
 DB 268 QQLLEPMKTHYMLKQLHREEVYLMQALISLSPDRGVLOHNVQLOBOFAITLKS 327
 QY 415 YIECNR-POPAHREFLKIMAMTELKRSINAOTQRLRIQDIHPFATPLMOELFG 469
 |||||
 DB 328 YIECNR-POPAHREFLKIMAMTELKRSINAOTQRLRIQDIHPFATPLMOELFG 383

RESULT 11
 Q91873 PRELIMINARY: PRT; 420 AA.
 ID 091873
 AC 091873
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE VITAMIN D RECEPTOR A.
 OS Paralicthys olivaceus (Flounder).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Pleuronectidae; Bothidae; Paralicthys.
 OX NCBI_TaxID=8255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RA Suzuki T., Suzuki N., Srivastava A.S., Kurokawa T.;
 RT "Identification of cDNAs encoding two subtypes of vitamin D receptor
 in flounder, Paralicthys olivaceus.";
 RL Biochem. Biophys. Res. Commun. 270:40-45(2000).
 DR EMBL; AB037674; BAA95016.1; -
 KM RECEPTOR.
 SQ SEQUENCE 420 AA; 47486 MW; 038FBF00D4F38067 CRC64;

Query Match 32.8%; Score 817; DB 13; Length 420;
 Best Local Similarity 43.1%; Pred. No. 1,8e-61;
 Matches 179; Conservative 70; Mismatches 144; Indels 22; Gaps 12;

QY 68 VNADE-EVGGPOICRVGDKATGYHNVMTGCGCGFFRRAMRNRLRCFPRKACET 126
 |||||
 DB 11 VGPDEFRNARICGVCGDKATGYHNVMTGCGCGFFRRAMRNRLRCFPRKACET 69

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OY 127 RKTROCCACLRKCSGKMKKIMSDAVERRALIKRKSERTGTLOPLAVOGLTEBO 186
D 70 KDNRRHCQACRLKRCIDIGMKKEFILTDEVOGKEKILKKEEAREAMPR-LINEQ 128
OY 187 RMIRRELDMAQKTEEDTFSHKFRP---GYLSSGCELPESLOAPSEBAKRSQVRK 243
D 129 ARMTSSLEAHMKKYDASDSEFSPREPVREGVTRASASRAASLSLSDASSDSFNHSP 188
OY 244 DLCLSKV---SLDRGEDSGVWYKPPADSGGKEIFSLPHAMADSTYFKGIIISPAVI 300
D 189 SV-DTKNFSLLMYODGA-----SPDSSEETKSLMPLHADVLSYIOVYIGFAKMT 243
OY 301 SYFDLPEDIOISLKGAFLCOLAFNTVFNAGTWECC--RLSYCLD-TAGGFOOL 357
D 244 PGFRLDLAEDQIALKSSAIEIIMRSNOSFSLSDMSWSCGGDPFKCINDVTKAGHLE 303
OY 358 LLEPNLKFHMLKLOLHEEYVLMQALISLSPDRGVLOHRYVLOLOQFATTKSITE 417
D 304 LLEPLVAFVGLKRLNHEEHVLMGICILSPDRGVODHARVQDLRLEALQAVIR 363
OY 418 CNRPOAHRELFLKIMAMTELRSINAQHTQ--RLLRIDHPR-ATPLMOELFG 469
D 364 IN--HFGGRLLVAKMIQKADLADSLNHEHSHKQYRSLSPQHSKQLTPLVLEVG 416

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RESULT 12
O9PTN2 PRELIMINARY; PRT: 453 AA.
AC O9PTN2;
DT 01-MAY-2000 (TREMUREL. 13, Created)
DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
DT 01-OCT-2000 (TREMUREL. 15, Last annotation update)
DE VITAMIN D RECEPTOR.
GN VDR.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7953;
RN [1]
RP SEQUENCE FROM N.A.
RA Koumenko A.P.;
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF164512; AAF21427.1;
DR HSSP: P20393; IAGY.
DR INTERPRO: IPR000324;
DR INTERPRO: IPR000336;
DR INTERPRO: IPR001628;
DR INTERPRO: IPR001723;
DR PFAM: PF00104; hormone_rec; 1.
DR PFAM: PF00105; zf-C4; 1.
DR PRINTS: PR00047; STROIDFINGER.
DR PRINTS: PR00350; VITAMINDR.
DR PRINTS: PR00398; STRDHOMOMER.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor.
SQ SEQUENCE 453 AA: 50765 MW; B52C82C185859F9C CRC64;

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Query Match 31.9%; Score 796; DB 13; Length 453;
Best Local Similarity 39.7%; Pred. No. 1.2e-59;
Matches 180; Conservative 76; Mismatches 165; Indels 32; Gaps 11;
OY 35 GEPANLEVPKESMNAHDFVHCEDTESVGRPSYNADEVGPOICRGCGKATGYFNV 94
D 11 GKSCEAGACSESVNGDATSLMDLMAVSTATGDDFDRNAPICGCGDKATGFHNA 70
OY 95 MTCSECKGFRAMKRNARLCPFKAGCETTRKTRQCAQRLKLESQKMKIMSD 154
D 71 MTCSECKGFRAMKRNARLCPFKAGCETTRKTRQCAQRLKLESQKMKIMSD 154
OY 155 EAVEERRALIKRKS---RTGTLOPLAVOGLTEBOHMLRELDMAQKTEEDTFSHKNF 211

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D 130 EYORRKLIMKKEEAREARKP---RLSDEQMLTNSLYEHNKTYDSDSEFVR 185
OY 212 RLP---GYLSSGCELPESLOAPSEBAKRS-----QVRKDLCLSKVLOLREGDSVW 262
D 186 RPPVREGPVTRASRAASLSLSDASSDSFNHSPESVDKLNFSLLMYODSGSPDS-- 243
OY 263 NYRPPADSGGKEIFSLPHAMADSTYFKGIIISPAKVSYFDLPEDIOISLKGAFL 322
D 244 ----SEEDQOSRLSMPLHADVLSYIOVYIGFAKMTPGFRLDLAEDQIALKSSAIEI 298
OY 323 COLPNTVFNAGTWECC--RLSYCLD-TAGGFOOLLEPNLKFHMLKLOLHEEY 379
D 299 IMRMSQSFSLSDMSWSCGGDPFKCINDVTKAGHLELLEPLVAFVGLKRLNHEEH 358
OY 380 VLMQALISLSPDRGVLOHRYVLOLOQFATTKSITECNRPOAHRELFLKIMAMTEL 439
D 359 VILMAICLSPDRGVODHARVQDLRLEALQAVIRIQ--HFGGRLLVAKMIQKADL 416
OY 440 RSINAQHTQ--RLLRIDHPR-ATPLMOELFG 469
D 417 RSLNEHSHKQYRSLSPQHSKQLTPLVLEVG 449

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RESULT 13
O9IB74 PRELIMINARY; PRT: 425 AA.
AC O9IB74;
DT 01-OCT-2000 (TREMUREL. 15, Created)
DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
DT 01-OCT-2000 (TREMUREL. 15, Last annotation update)
DE VITAMIN D RECEPTOR B.
GN VDRB.
OS Parachanna olivacea (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Perciformes; Pleuronectiformes;
OC Pleuronectidae; Boichidae; Parachanna.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-INTESTINE;
RA Suzuki T., Suzuki N., Sivasubava A.S., Kurokawa T.;
RT Identification of cDNAs encoding two subtypes of vitamin D receptor
RT in flounder, Parachanna olivacea.
RL Biochem. Biophys. Res. Commun. 270:40-45(2000).
DR EMBL: AB037673; BAA95015.1;
KW Receptor.
SQ SEQUENCE 425 AA: 48174 MW; 7B1D49CF4C2C65E9 CRC64;

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Query Match 31.7%; Score 790.5; DB 13; Length 425;
Best Local Similarity 41.6%; Pred. No. 3.3e-59;
Matches 179; Conservative 78; Mismatches 140; Indels 33; Gaps 13;
OY 61 SVPGPSYNADE-EGVGPOICRGCGKATGYFNVMTCECKGFRAMKRNARLCPFR 119
D 4 TVYTSLSASDEPDRNMPRICGCGDKATGFHNAHMAKCECKGFRAMKRNARLCPFR 62
OY 120 KGACETTRKTRQCAQRLKRCLESQKMKIMSDAVERRALIKRKS-----SERT 172
D 63 NGSCTITDNRHRCQACRLKRCYDIGMREFILTDEVOGKRLIRDEQARAEH 122
OY 173 GTOPLAVOGLTEBOHMLRELDMAQKTEEDTFSHKFRP---GYLSSGCELPESLOA 229
D 123 ARP---RLSDEQOSRLSMPLHADVLSYIOVYIGFAKMTPGFRLDLAEDQIALKSSAIEI 298
OY 230 PSREBAKRSQVRKDLCLSKV---LQLRGEDSGVWYKPPADSGGKEIFSLPHAMAD 285
D 179 LSDASSDSFNHSPESV-DTKNFSLLMYODGAS-----SPDSSEEGSFSKLPRLADL 233
OY 286 STYFKGIIISPAKVSYFDLPEDIOISLKGAFLCOLAFNTVFNAGTWECC--L 343

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Db 234 VSYIOLKIVIGFAMKIPGEFELTAEDQIALKSSAEVIMLNSQFNEJMSWSCGADPF 293
QY 344 SYCLEL-TAGGFOQLLEPMLEKFKHMKLQLOHEEYVLMQALISLSPDRPGVLOHRVVD 402
Db 294 KJOISVYTAGHTLELLELVKFOVGLKLNLOEEHVMALICLSPDRPGVQOCHARLE 353
QY 403 QLOEFAITLKSYIECNRPDPARHLEFLKIMAMTELKSINAOHQ--RLRIQDIHPF- 459
Db 354 ALQDRLESELTQAVIQH--HPGGRLLYAKMIQKLADRLSLNEHSHKQYRSLSPREHSMQ 411
QY 460 ATPIMQELFG 469
Db 412 LPPVLEVS 421

RESULT 14
Q90US1 PRELIMINARY; PRT: 358 AA.
ID Q90US1;
AC Q90US1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE NUCLEAR RECEPTOR.
GN CAR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR KYOTO, AND FISCHER;
RA Yoshinari K., Sueyoshi T., Moore R., Negishi M.;
RT "Sexually dimorphic nuclear translocation of receptor CAR and
RT induction of CYP2B1 gene by phenobarbital in rat livers.";
RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: A133095; AAF22567.1;
DR EMBL: A133095; AAF22566.1;
DR HSSP: P19793; 2N1L.
DR INTERPRO: IPR000324;
DR INTERPRO: IPR000536;
DR INTERPRO: IPR001628;
DR INTERPRO: IPR001723;
DR INTERPRO: IPR001728;
DR PRAM: PR00104; hormone_rec; 1.
DR PFAM: PF00105; zf-c4; 1.
DR PRINTS: PR00047; STROIDFINGER.
DR PRINTS: PR00350; VITAMINDR.
DR PRINTS: PR00398; STRDHOMOMER.
DR PRINTS: PR00546; THYROIDHOMR.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW RECEPTOR.
SQ SEQUENCE 358 AA; 40922 MW; 13691F49CAD8F1ED CRC64;

Query Match 29.2%; Score 729; DB 11; Length 358;
Best Local Similarity 40.3%; Pred. No. 4, 5e-54;
Matches 160; Conservative 61; Mismatches 122; Indels 54; Gaps 6;

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QY 312 ISILKGAPELCOLEBNTVENAFETWEGRLSCLEDTAG-GFOQLLEPMLEKFKHMK 370
Db 201 ISILKGAPELILSLNTTTCLOTONFPGCPICKEKEDAVNHGFOYELLELHFKTLK 260
QY 371 KLOLHEEYVLMQALISLSPDRPGVLOHRVVDLOBOFAITLKSYIECNRPDPARHLEFL 430
Db 261 RLQOEPEYALMAMALFSPDRPGVTOREBIDLOEVALILNNHIMEQSLQSLRFLYA 320
QY 431 KIAMTELKSINAOHQRLRIQDIHPFATPMOEL 467
Db 321 KIMGLAELRSINAYSSEIHRIOGLSAM-MPLUGEL 356

RESULT 15
Q90UH7 PRELIMINARY; PRT: 445 AA.
ID Q90UH7;
AC Q90UH7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE NUCLEAR OXYSTEROL RECEPTOR LXR-ALPHA (LXR-ALPHA).
GN NR1H3 OR LXR-ALPHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SV; TISSUE=LIVER;
RA Albert S., Steffensen K.R., Gustafsson J.A.;
RT "Cloning and characterization of nuclear oxysterol receptor genes LXR
RT and LXRb from mouse.";
RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: A132599; CAB51952.1; JOINED.
DR EMBL: A132600; CAB51952.1;
DR EMBL: A132601; CAB51923.1;
DR HSSP: P20393; 1A6Y.
DR MGD: MGI:1352462; Nr1h3.
DR INTERPRO: IPR000324;
DR INTERPRO: IPR000536;
DR INTERPRO: IPR000923;
DR INTERPRO: IPR001628;
DR INTERPRO: IPR001723;
DR INTERPRO: IPR001728;
DR INTERPRO: IPR003078;
DR PRAM: PF00104; hormone_rec; 1.
DR PFAM: PF00105; zf-c4; 1.
DR PRINTS: PR00047; STROIDFINGER.
DR PRINTS: PR00350; VITAMINDR.
DR PRINTS: PR00398; STRDHOMOMER.
DR PRINTS: PR00546; THYROIDHOMR.
DR PRINTS: PR01283; ECDYSTEROIDR.
DR PRINTS: PR01282; RETINOICACIDR.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
DR PROSITE: PS00196; COPPER_BLUE; UNKNOWN_1.
KW RECEPTOR.
SQ SEQUENCE 445 AA; 50476 MW; CC9A8DF38D935593 CRC64;

Query Match 20.2%; Score 504.5; DB 11; Length 445;
Best Local Similarity 30.4%; Pred. No. 7, 8e-35;
Matches 130; Conservative 85; Mismatches 142; Indels 71; Gaps 13;

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OY 171 ---RGTOPLGVOGLTEBORMMIRELMDAOMKTFPTTFSHEKNEFRLPGVLSGCELPESL 227
DB 190 VSPRVSSPPQVLPOLSPEDLMIERLVAACQCNRSFS----- 228
OY 228 QAPSRBEAKWQVRKDLCSLKVSLQLRGEGSVNNTKPPADSGKEIFSLPHADMT 287
DB 229 ---DRLRVTFW-PIAPD-----PQSHARQORFA---HTEIAI 260
OY 288 YMFKGIISPAKVISYFRDLPIDQISLKGAFELCOLFNTVEN--AETGTWEGRLSY 345
DB 261 VSVGEIYDPAKQLPGLQLSREDQIALKTSALIEVMLETSRYNPGSESITF-LKDSY 319
OY 346 CLEDTA-GGFQOLLLEPMLEKHYMLKQLCHEEYVLMQAISLESPPDRPGVLOHRVYDQ 404
DB 320 NREDEPAKAGLQVEFINPIFEFSRAMELQINDAEFALLIAISIFSADRPNVODOLOVERL 379
OY 405 OEQFALTLSYTECNRQPAHREFLKIMAMTELRSINAOHTORL--LRIDIHFEATP 462
DB 380 QHTYVEALHAYVINHPH--DRLMFPMDMLKLVSLTSSVHSEGVFALRLQD--KLPP 435
OY 463 LMQELFGI 470
DB 436 LISEIMDV 443

Search completed: February 18, 2001, 13:05:05
Job time: 6194 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 18, 2001, 13:43:38 ; Search time 51.75 seconds

(Without alignments)
295.171 Million cell updates/sec

Title: US-09-143-828-4

Perfect score: 2494
Sequence: 1 MVTYRTHHFKESGLRAPAIR.....QDIHPFAPPLMQLFGLTIGS 473

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2287	91.7	434	1	PXR_HUMAN
2	1779.5	71.4	431	1	PXR_MOUSE
3	1761.5	70.6	431	1	PXR_RAT
4	815.5	32.7	448	1	VDR_COTTA
5	815	32.7	451	1	VDR_CHICK
6	814	32.6	422	1	VDR_XENLA
7	801	32.1	423	1	VDR_RAT
8	792.5	31.8	422	1	VDR_MOUSE
9	789	31.6	424	1	VDR_BOVIN
10	789	31.6	427	1	VDR_HUMAN
11	768	30.8	348	1	NR13_HUMAN
12	729	29.2	358	1	NR13_RAT
13	725	29.1	358	1	NR13_MOUSE
14	500.5	20.1	461	1	NRH2_HUMAN
15	498.5	20.0	445	1	NRH3_MOUSE
16	496.5	19.9	445	1	NRH3_RAT
17	491.5	19.7	447	1	NRH3_HUMAN
18	489	19.6	446	1	NRH2_MOUSE
19	488	19.6	446	1	NRH2_RAT
20	457.5	18.3	757	1	ECR_LOCCU
21	455.5	18.3	395	1	ECR_PAROL
22	455	18.2	675	1	ECR_AEDAE
23	452.5	18.1	461	1	THB1_HUMAN
24	450	18.0	369	1	THB_CHICK
25	449	18.0	373	1	THB_RANCA
26	448	18.0	373	1	THB_XENLA
27	445	17.8	476	1	THB2_HUMAN
28	444.5	17.8	461	1	THB1_MOUSE
29	443	17.8	414	1	THB1_XENLA
30	443	17.8	461	1	THB1_RAT
31	442	17.7	475	1	THB2_MOUSE
32	439.5	17.6	579	1	NRD2_HUMAN
33	437	17.5	514	1	THB2_RAT

34	436	17.5	427	1	THA1_BRARE
35	434.5	17.4	878	1	ECR_DROME
36	434	17.4	416	1	THA1_PAROL
37	433	17.4	556	1	ECR_XANSE
38	428	17.2	448	1	RRB2_HUMAN
39	428	17.2	560	1	RORG_HUMAN
40	427.5	17.1	458	1	RRA_XENLA
41	427.5	17.1	576	1	NRD2_MOUSE
42	425.5	17.1	408	1	THA_CHICK
43	425	17.0	455	1	RRB_CHICK
44	424.5	17.0	411	1	THB1_SHEEP
45	424.5	17.0	536	1	ECR_CHITE

ALIGNMENTS

RESULT	1	STANDARD	PRT	434 AA
AC	PXR_HUMAN			
AC	075469:			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	ORPHAN NUCLEAR RECEPTOR PXR (PREGNANE X RECEPTOR) (ORPHAN NUCLEAR RECEPTOR PARL).			
GN	NR12 OR PXR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	(1)			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER:			
RX	MEDLINE-98395173; PubMed-9727070;			
RA	Lehmann J.M., McKee D.D., Watson M.A., Willson T.M., Moore J.T.,			
RA	Kliwer S.A.;			
RT	"The human orphan nuclear receptor PXR is activated by compounds that			
RT	regulates CYP3A4 gene expression and cause drug interactions.";			
RL	J. Clin. Invest. 102:1016-1023(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER:			
RX	MEDLINE-98445350; PubMed-9770465;			
RA	Bertilsson G., Heidrich J., Svensson K., Asman M., Jendeborg L.,			
RA	Sydney-Bachman M., Ohlsson R., Postlund H., Blomquist P.,			
RA	Barkenstein A.;			
RT	"Identification of a human nuclear receptor defines a new signaling			
RT	pathway for CYP3A induction.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 95:12208-12213(1998).			
CC	- FUNCTION: ORPHAN RECEPTOR. ITS NATURAL LIGAND IS PROBABLY			
CC	PREGNANE. BINDS TO A RESPONSE ELEMENT IN THE CYP3A4 GENE PROMOTER.			
CC	- SUBUNIT. FORMS A HETERODIMER WITH RXR.			
CC	- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	- TISSUE SPECIFICITY: EXPRESSED IN LIVER, COLON, AND SMALL			
CC	INTESTINE.			
CC	- INDUCTION: ACTIVATED BY NATURALLY OCCURRING STEROIDS SUCH AS			
CC	PREGENOLONE AND PROGESTERONE.			
CC	- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.			
CC	NR1 SUBFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: AF061056; AAC05436.1;			
DR	EMBL: AF084645; AAC64558.1;			
DR	MTX: 603065;			
DR	INTERPRO: IPR000324;			
DR	INTERPRO: IPR000536;			

DR INTERPRO: IPR001628; -
 DR INTERPRO: IPR001723; -
 DR PFAM: PF00104; hormone_rec; 1.
 DR PFAM: PF00105; zf-C4; 1.
 DR PRINTS: PR00047; STEROIDFINGER.
 DR PRINTS: PR00350; VITAMINDR.
 DR PRINTS: PR00398; STDRHORMONER.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 DR Receptor; transcription regulation; DNA-binding; Nuclear protein;
 zinc-finger.
 FT DNM_BIND 41 107 C4-TYPE ZINC FINGERS (TWO).
 FT ZN_FING 41 61 C4-TYPE.
 FT ZN_FING 77 102 C4-TYPE.
 FT ZN_FING 108 204 C4-TYPE.
 FT DOMAIN 205 434 HINGE.
 FT SEQUENCE 434 AA; 49761 MW; 1DF6A2AE3109CADA CRC64;

Query Match 91.7%; Score 2287; DB 1; Length 434;
 Best Local Similarity 99.8%; Pred. No. 6,9e-176;
 Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 40 LEVPRKSNHADVHCEDESVGPKPSVNADEVGPGQICRCGDKATGYHFWMTCEG 99
 DB 1 MEVPRKSNHADVHCEDESVGPKPSVNADEVGPGQICRCGDKATGYHFWMTCEG 60
 QY 100 CKGFERRAMKRNRLRCPFRKACETTRKTRROCOACRLKLESCKKEMINSDEAVEE 159
 DB 61 CKGFERRAMKRNRLRCPFRKACETTRKTRROCOACRLKLESCKKEMINSDEAVEE 120
 QY 160 RRAIKRRKSRGTGTPGVGLTEORPMIRIEMDAQMTFTTFSHFNRFLPGVLSS 219
 DB 121 RRAIKRRKSRGTGTPGVGLTEORPMIRIEMDAQMTFTTFSHFNRFLPGVLSS 180
 QY 220 GCELPESLOAPSRKANKSVORRDLCSLAVSLQREDSVWYKRPANSGKEIFSL 279
 DB 181 GCELPESLOAPSRKANKSVORRDLCSLAVSLQREDSVWYKRPANSGKEIFSL 240
 QY 280 PHMADMTYFKGISFAKYSYFRDLPIDQISLKGAFELCOLRFTVFAETGWE 339
 DB 241 PHMADMTYFKGISFAKYSYFRDLPIDQISLKGAFELCOLRFTVFAETGWE 300
 QY 340 CGRLSTCLEPTAGFQOLLEPMKFKHYMKKIQLEHEEYVLMQASISLSPDRPGVLOHR 399
 DB 301 CGRLSTCLEPTAGFQOLLEPMKFKHYMKKIQLEHEEYVLMQASISLSPDRPGVLOHR 360
 QY 400 VVQLOQOPATLTKSYTECHRPQAHRELFKLTAMLTLSINAQOTGLLTIQDIHP 459
 DB 361 VVQLOQOPATLTKSYTECHRPQAHRELFKLTAMLTLSINAQOTGLLTIQDIHP 420
 QY 460 ATPLMQELFGITGS 473
 DB 421 ATPLMQELFGITGS 434

RESULT 2
 PXR_MOUSE STANDARD; PRT; 431 AA.
 ID PXR_MOUSE
 AC 054915;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ORPHAN NUCLEAR RECEPTOR PXR (PREGNANE X RECEPTOR).
 GN NR112 OR PXR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=LIVER;
 RX MEDLINE=98149345; PubMed=9489701;
 RA Klierer S.A., Moore J.T., Wade L., Staudinger J.L., Watson M.A.,
 Jones S.A., McKee D.D., Oliver B.B., Willson T.M., Zetterstrom R.H.,

RA Perlmann T., Lehmann J.M.;
 RT "An orphan nuclear receptor activated by pregnanes defines a novel
 RT steroid signaling pathway.";
 RL Cell 92:73-82(1998)
 CC -1- FUNCTION: ORPHAN RECEPTOR, ITS NATURAL LIGAND IS PROBABLY
 CC PREGNANE. BINDS TO A RESPONSE ELEMENT IN CYP3A GENES PROMOTER.
 CC -1- SUBUNIT: FORMS A HETERODIMER WITH RXR.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1/PXR.1 (SHOWN HERE) AND
 CC 2/PXR.2; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- INDUCTION: ACTIVATED BY NATURALLY OCCURRING STEROIDS SUCH AS
 CC PREGNENOLONE AND PROGESTERONE, SYNTHETIC GLUCOCORTICOID AND
 CC ANTIGLUCOCORTICOID AND 16-ALPHA-CARBONITRILE (PCN).
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NR1 SUBFAMILY.

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DR EMBL: AF031814; AAC39964.1; -
 DR MGD: MGI:1337040; NR112.
 DR INTERPRO: IPR000324; -
 DR INTERPRO: IPR000536; -
 DR INTERPRO: IPR001628; -
 DR INTERPRO: IPR001723; -
 DR PFAM: PF00104; hormone_rec; 1.
 DR PFAM: PF00105; zf-C4; 1.
 DR PRINTS: PR00047; STEROIDFINGER.
 DR PRINTS: PR00350; VITAMINDR.
 DR PRINTS: PR00398; STDRHORMONER.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 DR Receptor; transcription regulation; DNA-binding; Nuclear protein;
 zinc-finger; Alternative splicing.
 FT DNM_BIND 38 104 C4-TYPE ZINC FINGERS (TWO).
 FT ZN_FING 38 58 C4-TYPE.
 FT ZN_FING 74 99 C4-TYPE.
 FT ZN_FING 105 201 C4-TYPE.
 FT DOMAIN 202 431 HINGE.
 FT VASPLIC 171 211 MISSING (IN ISOFORM 2).
 SO SEQUENCE 431 AA; 49567 MW; F592AF91F689329E CRC64;

Query Match 71.4%; Score 1779.5; DB 1; Length 431;
 Best Local Similarity 77.2%; Pred. No. 3.1e-135;
 Matches 332; Conservative 42; Mismatches 55; Indels 1; Gaps 1;

QY 42 VPRKSNHADVHCEDESVGPKPSVNADEVGPGQICRCGDKATGYHFWMTCEG 101
 DB 1 MPRKSNHADVHCEDESVGPKPSVNADEVGPGQICRCGDKATGYHFWMTCEG 59
 QY 102 GFFRRAMKRNRLRCPFRKACETTRKTRROCOACRLKLESCKKEMINSDEAVEER 161
 DB 60 GFFRRAMKRNRLRCPFRKACETTRKTRROCOACRLKLESCKKEMINSDEAVEER 119
 QY 162 ALIKRRKSRGTGTPGVGLTEORPMIRIEMDAQMTFTTFSHFNRFLPGVLSSG 221
 DB 120 ALIKRRKSRGTGTPGVGLTEORPMIRIEMDAQMTFTTFSHFNRFLPGVLSSG 179
 QY 222 ELPELSQAPSRKANKSVORRDLCSLAVSLQREDSVWYKRPANSGKEIFSLPH 281
 DB 180 ELPELSQAPSRKANKSVORRDLCSLAVSLQREDSVWYKRPANSGKEIFSLPH 239
 QY 282 MADMTYFKGISFAKYSYFRDLPIDQISLKGAFELCOLRFTVFAETGWE 341
 DB 240 MADMTYFKGISFAKYSYFRDLPIDQISLKGAFELCOLRFTVFAETGWE 299
 QY 342 RLSTCLEPTAGFQOLLEPMKFKHYMKKIQLEHEEYVLMQASISLSPDRPGVLOHRV 401
 DB 302 RLSTCLEPTAGFQOLLEPMKFKHYMKKIQLEHEEYVLMQASISLSPDRPGVLOHRV 359

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OY      42 VRPKESWNHADFVHCEDTIESIPGKPSVNADDEFGGGPQICRVCCKATGYHENWNTCEGCK 101
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DR      01-FEB-1996 (Rel. 33, Created)
DR      01-FEB-1996 (Rel. 33, Last sequence update)
DR      30-MAY-2000 (Rel. 39, Last annotation update)
DE      VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
GN      VDR OR NR111.
OS      Coturnix coturnix japonica (Japanese quail).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Coturnix.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=CHORIOALLANTOIC MEMBRANE;
RX      MEDLINE=95062315; PubMed=7972109;
RA      Elaroussi M.A., Prah J.M., Deluca H.F.;
RT      "The avian vitamin D receptors: primary structures and their
RL      origins";
RL      Proc. Natl. Acad. Sci. U.S.A. 91:11596-11600(1994).
CC      -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
CC      THE EXPRESSION OF HORMONE SENSITIVE GENES.
CC      -1- SUBCELLULAR LOCATION: NUCLEAR.
CC      -1- SUBCELLULAR LOCATION: TWO FORMS (A AND B) ARE PRODUCED BY USE OF
CC      ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
CC      -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC      A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC      -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC      NR1 SUBFAMILY.
CC      -----
CC      THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
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CC      ENTITIES REQUIRES A LICENSE AGREEMENT (SEE http://www.isb-sib.ch/announce/
CC      OR SEND AN EMAIL TO license@isb-sib.ch).
CC      EMBL: U12641; AA56725.1.
DR      HSSP: P03372; 1HCO
DR      INTERPRO: IPR000324;

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DR INTERPRO: IPR000536; -
 DR INTERPRO: IPR001628; -
 DR PFAM: PF00104; hormone_rec. 1.
 DR PFAM: PF00105; zf-C4; 1.
 DR PRINTS: PR00047; STEROIDFINGER.
 DR PRINTS: PR00350; VITAMINDR.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 zinc-finger; Alternative initiation.
 KM CHAIN 1 448 VITAMIN D3 RECEPTOR, ISOFORM A.
 FT CHAIN 26 448 VITAMIN D3 RECEPTOR, ISOFORM B.
 FT INIT_MET 26 26 FOR ISOFORM B.
 FT DNA_BIND 44 109 C4-TYPE ZINC FINGERS (TWO).
 FT ZN_FING 80 64 C4-TYPE.
 FT ZN_FING 104 104 C4-TYPE.
 FT DOMAIN 110 212 HINGE.
 FT DOMAIN 213 448 LIGAND-BINDING.
 SQ SEQUENCE 448 AA; 50668 MW; FCFIFC3DEAEAF3E CRC64;

Query Match 32.7%; Score 815.5; DB 1; Length 448;
 Best Local Similarity 40.9%; Pred. No. 5.2e-58;
 Matches 179; Conservative 72; Mismatches 154; Indels 33; Gaps 10;

QY 56 CEDTE--SVPKPSVNADE-EVGGPOICRYOGDKATGHHNVMTCEGCKGFFRRMKN 111
 DB 16 CEGSLQSSDMETPAVGPEDRNVPICGVGDRATGFHNMATCEGCKGFFRRMKN 75
 QY 112 ARLRPFKRGACETRRROCOACRLKCLESGKKKMSDAVERALLIRKKSER 171
 DB 76 AMFTCPF-SGCKKITKDRRCOCARLKCVDIGMKKEFILTDEYORKRREMIIRKEE 134
 QY 172 TGTPLVGOGLTEORRMIRELDAOMKTEFTDTSHEFNRLP-----GYL 217
 DB 135 ALKESLAKR-LSEBQAKINILAEHNTFTTSDFKFPFRKRSSTATHSSSV 193
 QY 218 SSGCELPESLQAPSRREAAKMSQVRKDCSLKVSQLRGEGDSVWNTKPPADSGKEIFS 277
 DB 194 SODFSESDSNVFGSDAGAFPEPMEPQFNSNLDSESDSPSMNTELPH-----LP 246
 QY 278 LLPHADSTYMKGIIFAVYISFRDLPIEDQISLKGAFELCOLRFTVYNAETG 337
 DB 247 MLPHLADVSYSLQVIFAKMIPGFRDLTAEDQIALKSAIVIMLRNSQSTMDMS 306
 QY 338 WECCGR--LSYCLDE-TAGGFOOLLLEPAIKFHYMLKQLHEEYVLMQALSPSPDPG 394
 DB 307 WTGSGNDKRYKVDYTGAGHMDLEPLVRFQVGLKRLNLEEHVLMALICISPPDPG 366
 QY 395 VLQHRVVDQLEQFAITIKSYTECNRPQAPARFLFLKIMALTSLRSTNAQHQ--RLR 452
 DB 367 VQDSIVESIQRDLSDTLQTYIRCHNPPGSRLLYAKMIQKLDLRLSNEHSKQYCLS 426
 QY 453 IODIHPF-ATPLMQELPG 469
 DB 427 FQPEHSMQLTPLVLEVFG 444

RESULT 5
 VDR_CHICK STANDARD; PRT; 451 AA.
 AC 04392;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
 GN VDR OR NRI11.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LEGHORN; TISSUE-KIDNEY;

RX MEDLINE-97223363; PubMed-9056239;
 RA Lu Z., Hanson K., Deluca H.F.;
 RT "Cloning and origin of the two forms of chicken vitamin D receptor.";

RL Arch. Biochem. Biophys. 339:99-106(1997).

RN

RP SEQUENCE OF 45-114 FROM N.A.

RA MEDLINE-87149040; PubMed-3029866;

RX McDonnell D.P., Mangelsdorf D.J., Pike J.W., Haussler M.R.,

RA O'Malley B.W.;

RT "Molecular cloning of complementary DNA encoding the avian receptor

for vitamin D.";

RL Science 235:1214-1217(1987).

CC -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING

THE EXPRESSION OF HORMONE SENSITIVE GENES.

CC -1- SUBCELLULAR LOCATION: NUCLEAR.

CC -1- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) ARE PRODUCED BY USE OF

ALTERNATIVE INITIATION CODONS.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN KIDNEY AND INTESTINE.

CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,

A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

CC NRI SUBFAMILY.

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or send an email to license@sib-sib.ch).

CC EMBL: AF01356; AAB62579.1; -

DR INTERPRO: IPR000324; -

DR INTERPRO: IPR000536; -

DR INTERPRO: IPR001628; -

DR PFAM: PF00104; hormone_rec. 1.

DR PFAM: PF00105; zf-C4; 1.

DR PRINTS: PR00047; STEROIDFINGER.

DR PRINTS: PR00350; VITAMINDR.

DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.

KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;

KW Zinc-finger.

FT CHAIN 1 451 VITAMIN D3 RECEPTOR, FORM A.

FT INIT_MET 15 15 VITAMIN D3 RECEPTOR, FORM B.

FT DNA_BIND 47 112 C4-TYPE ZINC FINGERS (TWO).

FT ZN_FING 47 67 C4-TYPE.

FT ZN_FING 83 107 C4-TYPE.

FT DOMAIN 113 215 HINGE.

FT DOMAIN 216 451 LIGAND-BINDING.

SQ SEQUENCE 451 AA; 51299 MW; 2078B6A6C8DBE5FC CRC64;

Query Match 32.7%; Score 815; DB 1; Length 451;
 Best Local Similarity 40.0%; Pred. No. 5.8e-58;
 Matches 181; Conservative 75; Mismatches 155; Indels 42; Gaps 11;

QY 47 SWNH-----ADVFACEDTESVPGKPSVNADEVEGGPOICRYOGDKATGHHNVMT 96
 DB 7 SWDEQOQSNAAVLPDADMDTVAASTSLP-DPAGDFRN--PRICGVCDRATGFHNMAT 63
 QY 97 CEGCKGFFRRMKNRANRLAPPRKACETTRTRROCOACRLKCLESGKKKEMMSDEA 156
 DB 64 CEGCKGFFRRMKNRANRLAPPRKACETTRTRROCOACRLKCLESGKKKEMMSDEA 122
 QY 157 VEERRALLIRKKSERTGTPGLVGOGLTEORRMIRELDAOMKTEFTDTSHEFNRLP-- 214
 DB 123 VQRKRMILKKEEELAKSLKPR-LSEBQAKVIDTLAEHNTFTTSDFKFPFRKRSSTATHSSSV 181
 QY 215 -----GVSSGCELPESLQAPSRREAAKMSQVRKDCSLKVSQLRGEGDSVW 262
 DB 182 SKFSSRMATSSSVSODFSESDSNVFGSDAFAPPEPMEPQFNSNLDSESDSPSM 241

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QY 263 NKKPPADSGGKIFSLPHMADMYMFKGISPAKVISYERDLEIEDQISLKGAFEL 322
DB 242 NIELH-----LPLMLADLVSYSIQKVIQFAKMIPEFQDLAEDIALKSSAIEV 294
QY 323 COLRENTVNAETGWEGR--LSYCLEL-TAGGFQOLLEPMKLFHMKLQLEHEEY 379
DB 295 IMLRSQSTYMDMSTGCSNDKFKVSDVYQAGHSMDLEPLVAFQVGLKLNHEEY 354
QY 380 VLMQAIISLSPDRPGVLAHRVVDQLOEQFATLKSYIECNRPQAPARFLFKIMAMTEL 439
DB 355 VLMACILSPDRPGVQDLSVESIQDRISDLQYIRCRHPPPSRLLYAKMIOKLADL 414
QY 440 KSIINAQHTQ--RLRIQDIHF-APPLMOELFG 469
DB 415 RSLNEHSKQYRCLSTFOPEHSMQPLVLEVFG 447

RESULT 6
VDR_XENIA STANDARD: PRT: 422 AA.
AC 013124;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
GN VDR OR NR11.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Piplidae;
OC Xenopodinae; Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RX MEDLINE-97307679; PubMed-9165021;
RA Li Y.C., Bergwitz C., Jueppner H., Demay M.B.;
RT Cloning and characterization of the vitamin D receptor from Xenopus
RT laevis.
RL Endocrinology 138:2347-2353(1997).
CC -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
CC THE EXPRESSION OF HORMONE SENSITIVE GENES.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: DETECTED IN ALL THE TISSUE EXAMINED. HIGHEST
CC LEVEL IN SMALL INTESTINE AND SKIN.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT STAGE 13. INCREASES
CC GRADUALLY AND PEAKS AT STAGE 57-61 THEN DECREASES TO THE LEVEL
CC SEEN IN ADULT.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NRI SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U91846; AAB58585.1;
DR INTERPRO: IPR000324;
DR INTERPRO: IPR000536;
DR INTERPRO: IPR001628;
DR PFAM: PF00105; hormone_rec.1.
DR PRINTS: PR00047; STEROIDFINGER.
DR PRINTS: PR00350; VITAMINDR.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR.1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
FT DNA_BIND 25 90 C4-TYPE ZINC FINGERS (TWO).
FT ZN_FING 25 45 C4-TYPE.
FT ZN_FING 61 85 C4-TYPE.

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FT DOMAIN 91 188 HINGE.
FT DOMAIN 189 422 LIGAND-BINDING.
SQ SEQUENCE 422 AA; 48188 MW; CBA9F2541FEE9D5 CRC64;

Query Match 32.6%; Score 814; DB 1; Length 422;
Best Local Similarity 41.1%; Pred. No. 6,4e-58;
Matches 172; Conservative 74; Mismatches 123; Indels 50; Gaps 10;

QY 77 POCROGDKATGYHNWMTCEGCKGFFRRAMRNRLACPFKGCCELTRRRCQAC 136
DB 22 PRICGCGDAGTGFHFNAMTCGCKGFFRRSMKRMFTCPF-NGDCRTTKNRRRCQSC 80
QY 137 RLKCLSGCKKIMINSDEAVERRALIRKRSERGTOTPLQVGTGECORMIRELMA 196
DB 81 RLKRCVDIGMKREFILDEYQKROMINKRSEELKSMRK-ISDQCKMIDILERA 139
QY 197 QMTPTTFSEHFNRLPGVLSGCELPESLQAPSFEAKMSQVRKDCSLKVSQIQLG 256
DB 140 HRTFTDTYEDFNKFR-----PVRENVDPEFRITR-----SSSVHTQG 178
QY 257 ---EDGSVMYKRPADS-----GGRK-IFSLPHMADMYMFKGIS 295
DB 179 SPESDSVFTSPDSSEHGFFSASLFGQETYSWGKSGSELSLPHIADLVSYSIQKIIG 238
QY 296 FAKVISYFRLPIEDQISLKGAFELCOLRENTVNAETGWEGR--LSYCLEL-TAG 352
DB 239 FAKMIFRFLIMEDQIALKSVIYIMKRSQSLDMSYTCSEDFKRVDTQTA 298
QY 353 GFOQLLEPLKPFHYMKLQLEHEEYVLMQAIISLSPDRPGVLAHRVVDQLOEQFATL 412
DB 299 GHNMLELPLKPFQVQGLKDLHEEHLVLMACILSPDRPGVLAHRVVDQLOEQFATL 358
QY 413 KSYIECNRPQAPARFLFKIMAMTELRSINAQHTQRLRIQDIHFPA---IPMOELF 468
DB 359 QTYILCKHPGSGRLLYAKMIOKLADLSLNEHSKQYRSISFLPHSMKLTPLMLEVF 417

RESULT 7
VDR_RAT STANDARD: PRT: 423 AA.
AC P13053;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
GN VDR OR NR11.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89071726; PubMed-2849110;
RA Burmeister J.K., Wiese R.J., Maeda N., Deluca H.F.;
RT Structure and regulation of the rat 1,25-dihydroxyvitamin D3
RT receptor.
RL Proc. Natl. Acad. Sci. U.S.A. 85:9499-9502(1988).
RN [2]
RP SEQUENCE OF 58-423 FROM N.A.
RX MEDLINE-88124963; PubMed-2829212;
RA Burmeister J.K., Maeda N., Deluca H.F.;
RT Isolation and expression of rat 1,25-dihydroxyvitamin D3 receptor
RT cDNA.
RL Proc. Natl. Acad. Sci. U.S.A. 85:1005-1009(1988).
CC -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
CC THE EXPRESSION OF HORMONE SENSITIVE GENES.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NRI SUBFAMILY.
CC -----
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QY 417 ECNRPQAHFLFLKMTLRSINAOHQ--RLRIQDHPF-APPIMQELFG 469
 DB 363 RCHNPPGSHOLYAKMIQKLADLRSLNEHSHKQYRSLSPENSMKLTPLVLEVG 418

RESULT 9
 VDR_BOVIN STANDARD; PRT: 424 AA.

ID VDR_BOVIN STANDARD; PRT: 424 AA.
 AC 028037;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
 GN VDR OR NR1L1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97034797; PubMed-8880453;
 RA Nelbega H.L., Bosworth B.T., Reinhardt T.A.;
 RT "Nucleotide sequence of the bovine vitamin D3 receptor."
 RL J. Dairy Sci. 79:1313-1315(1996).
 CC -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
 CC THE EXPRESSION OF HORMONE SENSITIVE GENES.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NRI SUBFAMILY.
 CC
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL: U50200; AAB01543.1; -
 DR HSSP: P03372; IHCO.
 DR INTERPRO: IPR000324; -
 DR INTERPRO: IPR000536; -
 DR INTERPRO: IPR001628; -
 DR PFAM: PF00104; hormone_rec. 1.
 DR PFAM: PF00105; zf-C4. 1.
 DR PRINTS: PR00047; STROIDFINGER.
 DR PRINTS: PR00350; VITAMINDR.
 DR PROSITE: PS00031; NUCLEAR-RECEPTOR. 1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Phosphorylation. C4-TYPE ZINC FINGERS (TWO).
 FT DNA_BIND 21 86
 FT ZN_FING 21 41
 FT ZN_FING 57 81
 FT DOMAIN 87 188
 FT DOMAIN 189 424
 FT SEQUENCE 424 AA; 47957 MW; E9E24926CE38CB7D CMC64;

Query Match 31.6%; Score 789; DB 1; Length 424;
 Best Local Similarity 42.2%; Pred. No. 6,5e-56;
 Matches 174; Conservative 67; Mismatches 143; Indels 28; Gaps 9;

QY 77 PQCRCGCRKATYHNNWNTCECKGFFFRARAKRNALCPFRKACETTRKTRQCAQC 136
 DB 18 PRCGCGRATGCFHFNATCECKGFFFRSMKRNALFTCPF-NDCCRTTKRRHCAQC 76
 QY 137 RLKRCLESCKMKEMSDAVEREALIRKKKSERTGTQPLGVOGTEORRMIRELDA 196
 DB 77 RLKRCVDSCKMKFILTDEYQRRKRMILKKEEPLAKSLAPK-LSEQQRIAILLDA 135

QY 197 QMKTFTTSHFNKNRFLPGVLSG---CELPESLQAPSEERAKKSVQRKDL----- 246
 DB 136 HNKTYDPTYSDFCQFRPVRVNDGGSGHPSPNPSRHPT--FSGDSSSSCCSDHCITSSDM 193
 QY 247 ---SLKVLQRCGDSVWYKPPADSGCKEITSLPMDADMSTYFKGLISPAKYSVF 303
 DB 194 MDSSFSNLDISEDDSC-----DPSVTELSQSLMPLADLVYSTOKYIGAKMIPGR 248
 QY 304 RDLPIEDQISLKGAFELCOLRFNFTVNAETGTWECGRSLY---CLIEDTAGGFOQLLE 360
 DB 249 RDLSEQIVLKSASALEVIMLSNNEFTMDKSMTCGNDYKRYSDYTKASHLELIE 308
 QY 361 PMLFHYMLKRLQHEEYVLMQALISLSPDRPGVLOHRRVDOLOQOFATLTKSYTECNR 420
 DB 309 PLIKFOYGLKLNKHEEHVLMALICIVSPDRGVDALILEAIQRLSNTLOTYIRCRH 368
 QY 421 PQPHRRFLFKIMATLRSINAOHQ--RLRIQ-DHPFATPLMQELFG 469
 DB 369 PPSHLLYAKMIQKLADLRSLNEHSHKQYRSLSPENSMKLTPLVLEVG 420

RESULT 10
 VDR_HUMAN STANDARD; PRT: 427 AA.

ID VDR_HUMAN STANDARD; PRT: 427 AA.
 AC P11473;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
 GN VDR OR NR1L1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88217887; PubMed-2835767;
 RA Baker A.R., McDonnell D.P., Hughes M., Crisp T.M., Mangelsdorf D.J.,
 RA Hausler M.R., Pike J.W., Shine J., O'Malley B.W.;
 RT "Cloning and expression of full-length cDNA encoding human vitamin D
 RT receptor."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:3294-3298(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92379083; PubMed-1324736;
 RA Goto H., Chen K.S., Prah J.M., Deluca H.F.;
 RT "A single receptor identical with that from intestine/T47D cells
 RT mediates the action of 1,25-dihydroxyvitamin D-3 in HL-60 cells."
 RL Biochim. Biophys. Acta 1132:103-108(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LENS EPITHELIUM;
 RA Rae J.L., Shepard A.R.;
 RU Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9735582; PubMed-9212063;
 RA Miyamoto K., Kesterson R.A., Yamamoto H., Taketani Y., Nishiwaki E.,
 RA Tatsuji S., Inoue Y., Morita K., Takeda E., Pike J.W.;
 RT "Structural organization of the human vitamin D receptor chromosome
 RT gene and its promoter."
 RL Mol. Endocrinol. 11:1165-1179(1997).
 RN [5]
 RP SEQUENCE OF 24-90 FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD;
 RX MEDLINE-91210272; PubMed-1850412;
 RA Yu X.-P., Kocharla H., Husterer F.G., Manolagas S.C.;
 RT "Vitamin D receptor expression in human lymphocytes. Signal
 RT requirements and characterization by western blots and DNA
 RT sequencing."
 RL J. Biol. Chem. 266:7588-7595(1991).
 RN [6]
 RP VARIANTS ASP-33 AND GLN-73.
 RX MEDLINE-89072761; PubMed-2849209;

RA Hughes M.R., Malloy P.J., Krieback D.G., Kesteron R.A., Pike J.W.,
RA Feldman D., O'Malley B.W.;
RT "Point mutations in the human vitamin D receptor gene associated with
RL hypocalcemic rickets."; *Science* 242:1702-1705(1988).
RN [7]
RP VARIANT GLN-35.
RX MEDLINE=93163233; PubMed=8381803;
RA Yagi H., Ozono K., Miyake H., Nagashima K., Kurose T.,
RT "A new point mutation in the deoxyribonucleic acid-binding domain of
the vitamin D receptor in a kindred with hereditary
1,25-dihydroxyvitamin D-resistant rickets";
RL J. Clin. Endocrinol. Metab. 76:509-512(1993).
RN [8]
RP VARIANT GLN-50.
RX MEDLINE=91353584; PubMed=1652893;
RA Saito T., Ito M., Takeda E., Mahabubul Hug A.H.M., Naito E., Yokota I.,
RA Sone T., Pike J.W., Kuroda Y.;
RT "A unique mutation in the vitamin D receptor gene in three Japanese
patients with vitamin D-dependent rickets type II: utility of single-
strand conformation polymorphism analysis for heterozygous carrier
detection";
RL Am. J. Hum. Genet. 49:668-673(1991).
RN [9]
RP VARIANT GLN-80.
RX MEDLINE=91125370; PubMed=2177843;
RA Sone T., Marx S.J., Liberman U.A., Pike J.W.;
RT "A unique point mutation in the human vitamin D receptor chromosomal
gene confers hereditary resistance to 1,25-dihydroxyvitamin D3";
RL Mol. Endocrinol. 4:623-631(1990).
RN [10]
RP VARIANT GLN-80.
RX MEDLINE=94149129; PubMed=8106618;
RA Malloy P.J., Weisman Y., Feldman D.;
RT "Hereditary α 1,25-dihydroxyvitamin D-resistant rickets resulting
from a mutation in the vitamin D receptor deoxyribonucleic
acid-binding domain";
RL J. Clin. Endocrinol. Metab. 78:313-316(1994).
RN [11]
RP VARIANT LEU-274.
RX MEDLINE=93315633; PubMed=8392085;
RA Kristjansson K., Rut A.R., Hewison M., O'Riordan J.L.H., Hughes M.R.;
RT "Two mutations in the hormone binding domain of the vitamin D
receptor cause tissue resistance to 1,25 dihydroxyvitamin D3";
RL J. Clin. Invest. 92:12-16(1993).
RN [12]
RP VARIANTS GLU-45 AND ILE-47.
RX MEDLINE=95129267; PubMed=7828346;
RA Rut A.R., Hewison M., Kristjansson K., Luist B., Hughes M.R.,
RT "O-Riordan J.L.H.";
RL "Two mutations causing vitamin D resistant rickets: modelling on the
basis of steroid hormone receptor DNA-binding domain crystal
structures";
RT Clin. Endocrinol. (Oxf) 41:581-590(1994).
RN [13]
RP VARIANT ASP-46.
RX MEDLINE=96272879; PubMed=8675579;
RA Lin U.-T., Malloy P.J., Sakati N., Al-Ashwal A., Feldman D.;
RT "A novel mutation in the deoxyribonucleic acid-binding domain of the
vitamin D receptor causes hereditary 1,25-dihydroxyvitamin D-resistant
rickets";
RL J. Clin. Endocrinol. Metab. 81:2564-2569(1996).
RN [14]
RP VARIANTS SER-314 AND CYS-391.
RX MEDLINE=97120600; PubMed=8961271;
RA Whitfield G.K., Seiznick S.B., Hausler C.A., Hsieh J.-C.,
RA Galligan M.A., Jurutka P.W., Thompson P.D., Lee S.W., Zerwekh J.E.,
RA Hausler M.R.;
RT "Vitamin D receptors from patients with resistance to 1,25-
dihydroxyvitamin D(3): point mutations confer reduced transactivation
in response to ligand and impaired interaction with the retinoid X
receptor heterodimeric partner";
RL Mol. Endocrinol. 10:1617-1631(1996).

RT "Sexually dimorphic nuclear translocation of receptor CAR and
 induction of CYP2B1 gene by phenobarbital in rat livers."
 RT Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: BINDS AND TRANSACTIVATES THE RETINOIC ACID RESPONSE
 CC ELEMENTS THAT CONTROL EXPRESSION OF THE RETINOIC ACID RECEPTOR
 CC BETA 2 AND ALCOHOL DEHYDROGENASE 3 GENES (BY SIMILARITY).
 CC -1- SUBUNIT: HETERODIMER OF NR1I3 AND RXR (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NRI SUBFAMILY.
 CC
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 CC
 CC EMBL: AF133095; AAF22567.1; -
 CC EMBL: AF133094; AAF22566.1; -
 CC INTERPRO: IPR000324; -
 CC INTERPRO: IPR000536; -
 CC INTERPRO: IPR001628; -
 CC INTERPRO: IPR001723; -
 CC INTERPRO: IPR001728; -
 CC PFAM: PF00104; hormone_rec; 1.
 CC PFAM: PF00105; zf-C4; 1.
 CC PRINTS: PRO0047; STROIDFINGER.
 CC PRINTS: PRO0350; VITAMINDR.
 CC PRINTS: PRO0398; STRDHOMER.
 CC PRINTS: PRO0546; THYROIDHOMR.
 CC PROSITE: PS00031; NUCLEAR RECEPTOR; 1.
 CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 CC Zinc-finger; Activator.
 CC ZINC-BIND 21 86 C4-TYPE ZINC FINGERS (TWO).
 CC FT ZN_FING 21 41 C4-TYPE.
 CC FT ZN_FING 57 81 C4-TYPE.
 CC FT ZN_FING 57 81 C4-TYPE.
 CC SO SEQUENCE 358 AA; 40922 MW; 13691F49CAD8F1ED CRC64;

Query Match 29.2%; Score 729; DB 1; Length 358;
 Best Local Similarity 40.3%; Pred. No. 3.3e-51;
 Matches 160; Conservative 61; Mismatches 122; Indels 54; Gaps 6;
 QY 72 EVVGGPQICRVGDKATGHNVMTCGCGKFFRRAMRNALRCPPFRKACETIRKTR 131
 DB 13 EEEYGRNCVCGDRATGTHFALTCGCGKFFKRTVSKTIPICPF-AGRCYSKAQR 71
 QY 132 OCOACRLKRCESGKMKKIMSDEAVEERALLKRRKERTGTOTPLGVGLTEQRMAR 191
 DB 72 HCPACRLQCLNVMKRMKILTSALALARRARRRQAKSLQ---S-LSQCKELIQ 125
 QY 192 ELMDNQMTFTTTFHFHKKFRLPGVLSGCELPESLQAPREBAKWSQVRKDCSLKVS 251
 DB 126 TLIGATRHVGMFDQFVQFRPAXLFSH-HRPQPLAV----- 163
 QY 252 LQLRGDSVWVKKPPADSGGKEIFSLPHMADSTVWKGIIISPAKYVSPRDLPIED 311
 DB 164 -----VPLPLTHFADINTFMVQOLIKTKDLPRLSRSLMEDQ 200
 QY 312 ISLLGAFELCOLRFNTVFNATGTWECGRSLSYCLEDTAG-CFOQLLEPMKPFYMLK 370
 DB 201 ISLLGAFVLIHISINTFCLOTQNFPGRCYKMEADVHGFQYFLELIIHKKILK 260
 QY 371 KLQLEHEEYVLMQALISLSPDRPGVQLQHRVVDLOEQAPATLKSYTECNRPQAPHRFEL 430
 DB 261 RLQLOPEFVALMAAMALFSPDRPGVQLQREIIDLQLEVALILNNHIMEQSRISGRFLYA 320
 QY 431 KIMAMTELRSTNACHTORLLRIODIHPATPLMOEL 467
 DB 321 KIMGILLAEIRINSASVEIRHQGLSAM-MPLLEI 356

RESULT 13
 NR13 MOUSE STANDARD; PRT; 358 AA.
 AC 035627; 035628;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE ORPHAN NUCLEAR RECEPTOR NR1I3 (CONSTITUTIVE ANDROSTANE RECEPTOR)
 DE (CAR).
 GN NR1I3 OR CAR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP TISSUE-LIVER;
 RC MEDLINE-97442417; PubMed-9295294;
 RA Choi H.-S., Chung M., Tzameil I., Simha D., Lee Y.-K., Seol W.,
 RA Moore D.D.;
 RT "Differential transactivation by two isoforms of the orphan nuclear
 RT hormone receptor CAR."
 RL J. Biol. Chem. 272:23565-23571(1997).
 CC -1- FUNCTION: BINDS AND TRANSACTIVATES THE RETINOIC ACID RESPONSE
 CC ELEMENTS THAT CONTROL EXPRESSION OF THE RETINOIC ACID RECEPTOR
 CC BETA 2 AND ALCOHOL DEHYDROGENASE 3 GENES.
 CC -1- SUBUNIT: HETERODIMER OF NR1I3 AND RXR.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: CAR1 (SHOWN HERE) AND CAR2;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. CAR2 DOES NOT SEEM TO ACT AS
 CC A TRANSACTIVATOR.
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NRI SUBFAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: AF009327; AAC53349.1; -
 CC EMBL: AF009328; AAC53350.1; -
 CC MGD: MG1:1346307; NR1I3.
 CC INTERPRO: IPR000324; -
 CC INTERPRO: IPR000536; -
 CC INTERPRO: IPR001628; -
 CC INTERPRO: IPR001723; -
 CC INTERPRO: IPR001728; -
 CC PFAM: PF00104; hormone_rec; 1.
 CC PFAM: PF00105; zf-C4; 1.
 CC PRINTS: PRO0047; STROIDFINGER.
 CC PRINTS: PRO0350; VITAMINDR.
 CC PRINTS: PRO0398; STRDHOMER.
 CC PRINTS: PRO0546; THYROIDHOMR.
 CC PROSITE: PS00031; NUCLEAR RECEPTOR; 1.
 CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 CC Zinc-finger; Activator; Alternative splicing.
 CC ZINC-BIND 21 86 C4-TYPE ZINC FINGERS (TWO).
 CC FT ZN_FING 21 41 C4-TYPE.
 CC FT ZN_FING 57 81 C4-TYPE.
 CC FT VARSPLIC 281 286 DRPGV -> GFCMOS (IN ISOFORM CAR2).
 CC FT VARSPLIC 287 358 MISSING (IN ISOFORM CAR2).
 CC SO SEQUENCE 358 AA; 40894 MW; 4F07730FE78CADBC CRC64;

Query Match 29.1%; Score 725; DB 1; Length 358;
 Best Local Similarity 39.3%; Pred. No. 7e-51;
 Matches 157; Conservative 64; Mismatches 124; Indels 54; Gaps 6;
 QY 70 ADEEVGGPQICRVGDKATGHNVMTCGCGKFFRRAMRNALRCPPFRKACETIRKTR 129

```

Db 11 ASEEGRPNVCGDRAIGHFHALTEGCEGFRRTVSTIGPICPF-AGRECEVSAQ 69
QY 130 RROCCACRLKRCLESKEMKEMIMSDAVERRALTKRKSERTGQPLGVGLTEBORM 189
Db 70 RHHCPACRLQCLANVGMKMDLSBALALRAAOARAKASIQ-----LNOOOREL 123
QY 190 IRELMADOKMTFFDTFSHPKFRPLPGVLSGCCLEPSILOASREBAKMSQVRKDLCSLK 249
Db 124 VOILGATRHVGLPFDQVQFKPPAYL----- 151
QY 250 VSIQRGDSVMNKPAPDSGKEIFSLPHMADMTYFKGIISPAKYISFRDPIE 309
Db 152 -----PMHRRPQPRG--PVLPLTHFADINTFMVQOITKFTKDLPRSLTME 198
QY 310 DOISLKGAFELCOLRENTVFNAETGECRLSYCLDPTA-GGFOOLLLEPMLKFKHYM 368
Db 199 DOISLKGAAVEILHISLNTFCLOTEFPGCLCYKEDAVHAGFOYELESLIHFHKN 238
QY 369 LKTLQHEEYVLMQALISLESPRPGVQLQHRVVDQLOEPAITLKSYECNRDPAHRTL 428
Db 259 LKGLHDEPEVYLAATALESPDRPGVQLQREIDQLQEMALILNHHIMQOSRLQSL 318
QY 429 FLKIMAMTELRSINAOHTORLLRIODIHPRTPLMOEL 467
Db 319 YAKIMGLADLRSTINMAYTELQRELSAN-TELLGEI 356

RESULT 14
NRH2_HUMAN STANDARD; PRT; 461 AA.
AC P55055;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE OXYSTEROLS RECEPTOR LXR-BETA (LIVER X RECEPTOR BETA) (NUCLEAR ORPHAN
DE RECEPTOR LXR-BETA) (UBIQUITOUSLY-EXPRESSED NUCLEAR RECEPTOR) (NUCLEAR
DE RECEPTOR NER).
GN NRH2 OR LXR-B OR NUR OR NER.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-OSTEOSARCOMA;
RX MEDLINE=93011628; PubMed=7926814;
RA Shinar D.M., Endo N., Rutledge S.J., Vogel R., Rodan G.A., Schmidt A.;
RT "NER, a new member of the gene family encoding the human sterol
RT hormone nuclear receptor.";
RL Gene 147:273-276(1994)

-1- FUNCTION: ORPHAN RECEPTOR. BINDS PREFERENTIALLY TO DOUBLE-STRANDED
OLIGONUCLEOTIDE DIRECT REPEATS HAVING THE CONSENSUS HALF-SITE
SEQUENCE 5'-AGGTCA-3' AND 4-NT SPACING (DR-4).
-1- SUBUNIT: FORMS A HETERODIMER WITH RXR.
-1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-1- TISSUE SPECIFICITY: UBIQUITOUS.
-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
NRI SUBFAMILY.

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or send an email to license@isb-sib.ch).

EMBL: U07132; AAA61783.1; -
DR HSSP: P03372; LHCQ.
DR MIM: 600380; -
DR INTERPRO: IPR000536; -
DR INTERPRO: IPR001628; -
DR PFM: PF00104; hormone_rec; 1.

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DR PFM: PF00105; zf-C4; 1.
DR PRINTS: P00047; STROIDFINGER.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
FT ZINC_BIND 87 154 C4-TYPE ZINC FINGERS (TWO).
FT ZN_FING 87 107 C4-TYPE.
FT ZN_FING 125 149 C4-TYPE.
FT DOMAIN 231 461 LIGAND-BINDING (POTENTIAL).
FT DOMAIN 173 176 POLY-GLN.
FT DOMAIN 191 196 POLY-SER.
SQ SEQUENCE 461 AA; 51102 MW; 68CE3D9F9BC5C0BE CRC64;

Query Match 20 1%; Score 500.5; DB 1; Length 461;
Best Local Similarity 28.0%; Pred. No. 9.2e-33;
Matches 134; Conservative 93; Mismatches 153; Indels 99; Gaps 15;

QY 33 PRGPEANLE-VPRKESWNADVFHCEDETSVPGKSVNADDEVGSGPOICRGOKATGYH 91
Db 39 PGSPDDVGTCTDEASACSTDMVTPDEPERKRRKGPATLGHLCRCVCGDASGFH 98
QY 92 FNVATCEGCKGFFRRAMRNARLRCFPR-KGACETIRKTRRQCACRLKLESKREM 150
Db 99 YVNLSCGCKGFFRRSVYVGARFYACRGCGTCQMDAFMRRCQOCRLKCKEAGMRCQ 158
QY 151 IMSDEAVERRALTKRKSERTGTO---PLVQG----- 181
Db 159 VISEQIRKKK--IRKQOQESQSQSQSPVPGQSSSASGPGASPGSGSAGSGEGE 216
QY 182 ---LTEEQMMIRELMDAQMTFTTFHFNFRLPGVLSGCCLEPSILOASREBAKW 238
Db 217 GVQLRAQELMQQLVAQLOCNKRFS-----DQKTPW 252
QY 238 SVQRVDLSLKVSLQKREDSVMNKPAPDSGKEIFSLPHMADMTYFKGIISPAK 298
Db 253 P-----LGAD-----PQSRDAQRFA--HTELAISVQELVDPAK 287
QY 299 VISYFRDPIEDQSLKGAFFELCOLFNTVFNAETGTCW-----GLSTCLSD-TRGC 353
Db 268 QVPGILOQREDOJMLASTETIMLETARVHET--SCITFLDFTYSKDFHRAQ 344
QY 354 FQOLLLEPMKFRHWLKLQLOHEEYVLMQALISLESPRPGVQLQHRVVDQLOEPAITLK 413
Db 345 LQVERINPIFEFSRAMRLGLDADEYALLININFSADRVPVQSGVEALQGYEVAL 404
QY 414 SYIEENRQPAHRLFLKIMAMTELSINAOHTORL-LRIODIHPRTPLMOELFGI 470
Db 405 SYTRIKRPQDQLR--FPRMLKLVSLTSSVSHSEQVAFALRLD--KKLPLLSIEMDV 459

RESULT 15
NRH3_MOUSE STANDARD; PRT; 445 AA.
AC Q920Y9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE OXYSTEROLS RECEPTOR LXR-ALPHA (LIVER X RECEPTOR ALPHA) (NUCLEAR ORPHAN
DE RECEPTOR LXR-ALPHA).
GN NRH3 OR LXR-A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Chen T.E., Horluch M., Dzeu V.J.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: ORPHAN RECEPTOR. INTERACTION OF LXR ALPHA WITH RXR
CC SHIFTS RXR FROM ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN
CC ACTIVE LIGAND-BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES
CC THROUGH TARGET GENES DEFINED BY LXRES (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

```

CC -! SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NRI SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF085745; AAD16050.1; -.
 CC HSSP: P20393; 1A6Y.
 CC INTERPRO: IPR000536; -.
 CC INTERPRO: IPR001628; -.
 CC PRAM: PR00104; hormone_rec; 1.
 CC PRAM: PR00105; zf-C4; 1.
 CC PRINTS: PR00047; STROIDFINGER.
 CC PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 CC Zinc-finger.
 CC DNA_BIND 96 161 C4-TYPE ZINC FINGERS (TWO).
 CC FT DNA_BIND 96 116 C4-TYPE.
 CC FT ZN_FING 132 156 C4-TYPE.
 CC FT ZN_FING 132 156 C4-TYPE.
 CC SQ SEQUENCE 445 AA; 50417 MW; 1A426D38D935731 CRC64;

Query Match 20.0%; Score 498.5; DB 1; Length 445;
 Best Local Similarity 30.1%; Pred. No. 1.3e-32;
 Matches 129; Conservative 85; Mismatches 143; Indels 71; Gaps 13;

QY 57 EDTSVGRKSVNADVEYGGPQICRGVGDGKATGTHFNVTCEGCKGFFRRAMRNALRC 116
 DB 73 EPTLRPQKRKKGPAPKMGELSCVGDASGFHYNVLSCEGCKGFFRRSVTKGANYVC 132
 QY 117 PFRGACEITFKTRQOCARLKRKLESGMKEMMSDEAVEERALLIKRKE----- 170
 DB 133 -HSGCHPMGYMRKRCQECRLKRCQAGMEECVLSSEQIRLKK--LKRQEEQAQATS 189
 QY 171 --RTGTPLGVGLTEQRMRMIRELMDAOKTDTTFSHFKNRLPGVLSGCELPESL 227
 DB 190 VSPRVSPQVLPQLSPFQGLMIKILVAACQCNRSFS----- 228
 QY 228 QAPSRERAAKSVQRKDLCSIKVSLQLRGDEGSVMNTKPPADSGCKEISLPHMADMS 287
 DB 229 --DLKRVTPW-PIAPD-----PQSRERQQRFA--HFTETAI 260
 QY 288 YMFKGIISFAKVISFYRDLPIEDQISILKGAFFELCOLRFTVFN--AETGTWEGRLSY 345
 DB 261 VSVQEIYDFAKQPLQFQLSREDQIALKTSAIEVMLLETSRRYNPGSESITF-LKDFSY 319
 QY 346 CLEDTA--GGFQQLLEPMKTHYMLKTLQLEBEVYLMQAISLSPDRPGVLOHRYVDL 404
 DB 320 NREDFAKAGLQVEFINPFEFSRANNELOLNDAEFALLIAISISADPNVODLOVERL 379
 QY 405 QEQFATLKSTIECRPQARHFLFKIMAMLETLSINAQTORL--LRIDIHFPATP 462
 DB 380 QHTTYEALHAIVSYNHPRD--LMFPRKIMKIVSLRTISVSHSEQVFALRLQD--KILPP 435
 QY 463 LMOELFGI 470
 DB 436 LLSEIMDV 443

Search completed: February 18, 2001, 13:43:39
 Job time: 5859 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2001, 14:33:07 ; Search time 57.29 seconds

(without alignments)
560.604 Million cell updates/sec

Title: US-09-143-828-4

Perfect score: 2494

Sequence: 1 MVTFRTHHFKESGLRABAPR.....ODHPFAPPLMQLRGITGS 473

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR_66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	991.5	39.8	386	2	thyroid hormone re
2	817	32.8	420	2	vitamin D receptor
3	815.5	32.7	448	2	vitamin D receptor
4	801	32.1	423	2	1,25-dihydroxyvita
5	792.5	31.8	422	2	vitamin D receptor
6	790.5	31.7	425	2	vitamin D receptor
7	789	31.6	427	2	vitamin D receptor
8	789	31.6	427	2	vitamin D receptor
9	768	30.1	441	2	steroid hormone re
10	500.5	20.1	461	2	steroid hormone re
11	496.5	19.9	445	2	steroid hormone re
12	491.5	19.7	442	2	steroid hormone re
13	489	19.6	446	2	steroid hormone re
14	488	19.6	446	2	steroid hormone re
15	463	18.6	469	2	steroid hormone re
16	452.5	18.1	469	2	steroid hormone re
17	450	18.0	369	2	thyroid hormone re
18	450	18.0	369	2	thyroid hormone re
19	449	18.0	373	2	thyroid hormone re
20	448	18.0	373	2	thyroid hormone re
21	447.5	17.9	456	1	thyroid hormone re
22	447	17.9	456	1	thyroid hormone re
23	444.5	17.8	461	2	thyroid hormone re
24	443	17.8	373	2	thyroid hormone re
25	442	17.7	475	2	thyroid hormone re
26	440.5	17.4	464	2	thyroid hormone re
27	434.5	17.4	878	2	thyroid hormone re
28	434	17.4	416	2	thyroid hormone re
29	434	17.4	448	2	thyroid hormone re

30	432	17.3	444	2	retinoic acid rece
31	429	17.2	579	2	orphan nuclear hor
32	428	17.2	458	2	retinoic acid rece
33	428	17.2	459	2	retinoic acid rece
34	428	17.2	560	2	retinoic acid rece
35	427.5	17.1	576	2	nuclear receptor R
36	427	17.1	408	1	nuclear receptor R
37	425.5	17.1	408	1	thyroid hormone re
38	425	17.0	455	2	thyroid hormone re
39	424.5	17.0	536	2	retinoic acid rece
40	424.5	17.0	614	2	retinoic acid rece
41	424	17.0	458	2	thyroid hormone re
42	423	17.0	452	2	retinoic acid rece
43	423	17.0	578	2	retinoic acid rece
44	422	16.9	448	2	nuclear receptor R
45	422	16.9	955	4	retinoic acid rece

ALIGNMENTS

RESULT 1

thyroid hormone receptor homolog - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 20-May-1994 #sequence, revision 26-May-1995 #text, change 20-Sep-1999

C/Accession: S41497, S38486

R/Smith, D.P.; Mason, C.S.; Jones, E.A.; Old, R.W.

Nucleic Acids Res. 22, 66-71, 1994

A/Title: A novel nuclear receptor superfamily member in Xenopus that associates with

A/Reference number: S41497; MID:94173664

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1386 <SM>

A/Cross-references: EMBL:X75163; NID:g410517; PIDN:CA453006.1; PID:g410518

C/Suprafamily: unassigned erba-related proteins; erba transforming protein homolog;

C/Keywords: zinc finger

F;35-303/Domain: erba transforming protein homolog <ERBA>

Query Match 39.8%; Score 991.5; DB 2; Length 386;
Best Local Similarity 49.0%; Pred. No. 8.4e-70;
Matches 204; Conservative 59; Mismatches 104; Indels 49; Gaps 9;

QY	57	EDTSVPGKRSVNADEYVGGPOICRVGDKATGYHFNVTCEGKGFPRAMRNRLNC	116
DB	14	EEEDASNSCGTGEDDDGPKICRACGDRATGHEFAMTCBGCKGFPRAVRNRLSC	73
QY	117	PFRRACETTRKTRKOCACRLKRCESGKMKEMINSDEAVERRALIKR-KSERGTG	175
DB	74	PF-QNSCVINKSNRHCQACRLKCLDIGNKELINSDAVEGRALIKRHLTKLP	132
QY	176	PLVGQGLTEEDRMKIRLMDAOKTFPTTSKRNRLPGLVSSGCELPDLAPSSEA	235
DB	133	PPGA-SLTPGEQHLTDLVGAHRTFEDNFTSKNFP-----PIR--	171
QY	236	AKMSQVAKKDCSLKVSQLEGGDSVYNYKPPADSGKEIFSLPLPHADSTYMGIIIS	295
DB	172	-----RSSDPT---QEQATS--SEAFMLPHISDLVTYMIKGIIS	207
QY	296	FAKYISYFRDLPIDQSLKGAFLCQLRFTVFAETGTEGRLSYCLBDT-AGGF	354
DB	208	FAKMLPFKSLDIEDQIALKGSVAEVSIRFNTVFSDINTWCGPFTYDTDMFLAG	267
QY	355	QQLLEPMLKHYMLKQLQHEEYVLMQALSLFSPRPVQLHRYVDQEQEPAITLKS	414
DB	268	ROLLEPLVYRIRHMKRLINQSEEVYAMALSTFASDRPGCWEMKIQKQEHIALTLKD	327
QY	415	YIEENR-POPARRFLFKIMALFELRSINAGHRTORLRIODIHFPATPLMOELFG	469
DB	328	FLDSORPSPSPNRLIYRKIMECLTELTAVNDIHKQLLEIMDLPDAPLMAEYVFG	383

RESULT 2

JC7229

vitamin D receptor subtype a - Paralelchthys olivaceus

C:Species: Paralelchthys olivaceus

C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 18-Aug-2000

R:Suzuki, T.; Suzuki, N.; Srivastava, A.S.; Kurokawa, T.

A:Title: Identification of CDNA's encoding two subtypes of vitamin D receptor in flounder

A:Reference number: JC7229

A:Accession: JC7229

A:Molecule type: mRNA

A:Residues: 1-420 <SU2>

A:Cross-references: DDBJ:AB037673

A:Comment: This receptor is an important factor in calcium homeostasis and bone formation

C:Genetics:

A:Gene: vdr-a

A:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: bone; calcium transport; DNA binding; hormone receptor; intestine; vitamin D

Query Match 32.8%; Score 817; DB 2; Length 420;

Best Local Similarity 43.1%; Pred. No. 3.8e-56;

Matches 179; Conservative 70; Mismatches 144; Indels 22; Gaps 12;

68 VNAD-EEGSGPOICVGDGKATGYHFNVMTCGCKGFFRRAMKRNALPCFRKAGEIT 126

11 VGPDEFDMNAPRIGVCGDKATGFHFNMTCEGCKGFFRRAMKRNALPCFRKAGEIT 69

127 KTRRQOCARLKRKLESGMKNKEMSDAVERRALIKRKSERTGTPGVGLTEEG 186

70 KDNRRHOCACLRKICIDIGMKEFLTDEYQREKEMILKKEEAREARPR-LNEEQ 128

187 RMTRELDADQKTFDTTFHFKNRLP--GVLSGCELPESLQADSRERAAKWSQVR 243

129 ARMTSLVEAHKTYDASYDSFSEFRPVREGPYTRRSRAASLHSLSDSSSFNSPE 188

244 DLCSLKV---SLQSGEGSVWYKPPADSGKEIFSLPMAVMSTYMKGIISFAKYI 300

189 SV-DTKMNFSLMAYODGA-----SPDSSEMTKSLPMLADLVSTIQKIVGFMMKI 243

301 SYFDDLPEDQISLKGAFELCOLRNTVNAETGTEG--RLSYCLD-TAGGFQOL 357

244 PGFDLPEDQIALKSAIEIIMLRNSQSPLEDMSCGPGPKCINDVTKAGTLE 303

358 LLEPMKFNHMLKQLHEEYVLMQALISFSPRPGVLDHRVYDQLQEQPAITLKYIE 417

304 LLEPLVRFVGLKRLNHEEHVLMIGICLSPDRPGVDHARVEQLDRLPEALQAYIR 363

418 CNRPQAHRFLEFLKIMAMTELRSINOHQ--RLRLIODHPF-ATPLMOELFG 469

364 IN-HPGGRLLYAKMIQKRLADRLSLNEHRSQYSLSPFPHSKQLTPVLVEVFG 416

Db

RESULT 3

150451

vitamin D receptor isoform A - Japanese quail

C:Species: Coturnix coturnix japonica (Japanese quail)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999

C:Accession: 150451

R:Elaroussi, M.A.; Prah, J.M.; Deluca, H.F.

Proc. Natl. Acad. Sci. U.S.A. 91, 11596-11600, 1994

A:Title: The avian vitamin D receptors: primary structures and their origins.

A:Reference number: 150451; MUID:95062315

A:Accession: 150451

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-448 <ELAD>

A:Cross-references: EMBL:U12641; NID:9595500; PID:AAA56725.1; PID:9595501

C:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: zinc finger

F:42-362/Domain: erba transforming protein homology <ERBA>

Query Match 32.7%; Score 815.5; DB 2; Length 448;

Best Local Similarity 40.9%; Pred. No. 5.4e-56;

Matches 179; Conservative 72; Mismatches 154; Indels 33; Gaps 10;

56 CEOTE---SVGPSPVNADE-EVGGPOICRGDGTGYNVMTCEGCKGFFRRAMRN 111

16 CEEQELQSSDMETPANGTPEFDNAPRIGVCGDKATGFHFNMTCEGCKGFFRRAMRN 75

112 ARLRPFRRKAGEITRTRRQOCARLKRKLESGMKNKEMSDAVERRALIKRKSER 171

76 AMETCPF-SGDKITRDNRRHOCACLRKICVDIGMKEFLTDEYQREKEMILKKEE 134

172 TGTQPLGVGLTEEGQMMRELMDAQKTFDTTFHFKNRLP-----GYL 217

135 ALKESLPR-LSEEDQKVINILLEAHKHTFTYSDFNKFRPVRSKSSSTATHSSSV 193

218 SSGCELPESLQADSRERAAKWSQVRKDCSLKVSQLEGGDSVWYKPPADSGKEIFS 277

194 SQDFSESDNDVFGSDAFAPPEPMEPQFNSVDLSESDSPSNILPH-----LP 246

278 LLEPMKFNHMLKQLHEEYVLMQALISFSPRPGVLDHRVYDQLQEQPAITLKYIE 337

247 MLEPLADLVSTIQKIVGFMMKI-PGRDLTADQIALKSAIEIIMLRNSQSPLEDMSC 306

338 WEGGR--LSYCLD-TAGGFQOLLEPMKFNHMLKQLHEEYVLMQALISFSPRPG 394

307 WTGGSNDFTYKYSVDTQAGSHNDLEPLVRFVGLKRLNHEEHVLMIGICLSPDRPG 366

395 VLQHRVDDQLQEQMMRELMDAQKTFDTTFHFKNRLPFLKIMAMTELRSINOHQ--RLRL 452

367 VODTSLVESIQRLSPDTLOTYTRCHRPPEGSKLYAKMIQKRLADRLSLNEHRSQYR 426

453 IODIHPF-ATPLMOELFG 469

427 FQPEHSMQLTPVLVEVFG 444

Db

RESULT 4

A31761

1,25-dihydroxyvitamin D-3 receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Sep-1999

C:Accession: A31761; A31367

R:Burnester, J.K.; Wiese, R.J.; Maeda, N.; Deluca, H.F.

Proc. Natl. Acad. Sci. U.S.A. 85, 9499-9502, 1988

A:Title: Structure and regulation of the rat 1,25-dihydroxyvitamin D-3 receptor.

A:Reference number: A31761; MUID:89071726

A:Accession: A31761

A:Molecule type: mRNA

A:Residues: 1-423 <BRU>

A:Cross-references: GB:J04147; GB:J03630; NID:9203956; PIDN:AAA1089.1; PID:9203957

R:Burnester, J.K.; Maeda, N.; Deluca, H.F.

Proc. Natl. Acad. Sci. U.S.A. 85, 1005-1009, 1988

A:Title: Isolation and expression of rat 1,25-dihydroxyvitamin D-3 receptor cDNA.

A:Reference number: A31367; MUID:88124963

A:Accession: A31367

A:Molecule type: mRNA

A:Residues: 1-423 <BRU>

C:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: DNA binding; transcription regulation; zinc finger

F:22-337/Domain: erba transforming protein homology <ERBA>

F:24-44/Region: zinc finger

F:60-84/Region: zinc finger

Query Match 32.1%; Score 801; DB 2; Length 423;

Best Local Similarity 42.0%; Pred. No. 6.8e-55;

Matches 172; Conservative 75; Mismatches 135; Indels 28; Gaps 9;

77 PQICVCGDKATGYHFNVMTCGCKGFFRRAMKRNALPCFRKAGEITRTRRQOCAC 136

[illegible]

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RESULT      5
PC4019
vitamin D receptor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Sep-1995
C:Accession: PC4019
R:Name1, Y.: Kawada, T.; Fukuwatari, T.; Ono, T.; Kato, S.; Sugimoto, E.
Gene 152, 281-282, 1995
A:Title: Cloning and sequencing of the gene encoding the mouse vitamin D receptor
A:Reference number: PC4019; MID:95137405
A:Accession: PC4019
A:Molecule type: mRNA
A:Residues: 1-422 <KAA>
A:Cross-references: DBJ: D31369; NID: g699618; PIDN: BAA06737.1; PID: d1007311; PID: c
C:Superfamily: unassigned era- related proteins; era transforming protein homolog
C:Keywords: DNA binding; zinc finger
F:22-336/Domain: era transforming protein homology <ERBA>
F:24-89/Domain: DNA binding #status predicted <BN>
F:191-422/Region: vitamin D binding #status predicted

```

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Query Match 31.8%; Score 792.5; DB 2; Length 422;
Best Local Similarity 41.8%; Pred. No. 3.1e-54;
Matches 174; Conservative 74; Mismatches 127; Indels 41; Gaps 11

QY 77 PQCRCVCGDMKATGYHFNVTMCCEGCGFFFRAMRNRLALCPFKKACETITKTRROCCAC 136
   1: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 PRCGCGGDBRATYFHNNTATCEGCKCFPRSMRKALITCFP-NGSCRITKDRRRCCAC 79
   1: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 137 RLKRCLESGKKMKMINSDEAVEERALLIKRKKSERTGTPLGVQGITEDQRMIRLELMA 196
   1: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 80 RLKRCVDIGMKRFILITLDEVOQRKREIMKMKREALNKSRLRK-LSSEQHITALLDA 138
   1: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 197 QMFTPTTSHFKNRFLP--GVLSGCELP-----ESLQAPSR--EAAKMS 239
   1: || | || | || | || | || | || | || | || | || | || | || | || |
Db 139 HHKTYDPTVADFPPIRADVSTGSGSPRLTSGDSSNSDITPESLDMMEAPAS 198
   1: || | || | || | || | || | || | || | || | || | || | || | || |

QY 240 QVKKDLCSLKVSLQNGEDGSVMNKPAPNADSGGKEIFSLPLHMDASTYFKGLISPAKY 299
   1: || | || | || | || | || | || | || | || | || | || | || | || |
Db 199 TM--DL-----NEEGS---DDPSVTLDISPISMLPHADLVYSISKVIGPAMA 242
   1: || | || | || | || | || | || | || | || | || | || | || | || |

QY 300 ISYFRDLPIDEDISLKGAFELCOLFNFVFNALNETWDECGRLSYCLEDT---AGGFOQ 356
   1: || | || | || | || | || | || | || | || | || | || | || | || |
Db 243 IPGFRDLTSDQIVLTKSSAIEVIMLRNSQSFIMDMDSMCGGQDYKIDITIDVSRAGHTL 302
   1: || | || | || | || | || | || | || | || | || | || | || | || |

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OY 357 ILLEMLFHEFMKRLDHEEEYVMAISFSDRGVLOHRAVDLOJOFATLTSYI 418
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 303 ELIELIFCVGKLNLNHEEHVLAIVACVSDRGVODAKVLEIOBRLSTIOTYI 362Z
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 417 EGNRPQAHFFELIKYMLAMLELISINAOHQ--RLRIODIHDF-ATPDLQOEFG 469
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 363 RCRHPPFSHQVYAKMIKLDLMSINDEHSKQYRSLSTFQENSMKLTPLVLEVFG 418
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 6
JC7230
vitamin D receptor subtype b - Paraliichthys olivaceus
C.Species: Paraliichthys olivaceus
C.Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 18-Aug-2000
C.Accession: JC7230
R.Suzuki, T.; Suzuki, N.; Srivastava, A.S.; Kurokawa, T.
Biochem. Biophys. Res. Commun. 270, 40-45, 2000
Affile: Identification of cDNAs encoding two subtypes of vitamin D receptor in flounn
A.Reference number: JC7229
A.Accession: JC7230
A.Molecule type: mRNA
A.Residues: 1-425 <STU>
A.Cross-references: DDBJ:AB037674
A.Experimental source: Intestine
C.Comment: This receptor is an important factor in calcium homeostasis and bone forma
C.Genetics:
A.Gene: vdrnb
C.Superfamily: unassigned extra-related proteins: extra transforming protein homology
C.Keywords: bone; calcium transport; DNA binding; intestine; vitamin D

Query Match	34.78;	Score 790.5;	DB 2;	Length 425;
Best Local Similarity	45.68;	Pred. No. 4.5e-54;		
Matches 179;	Conservative 78;	Mismatches 140;	Indels 33;	Gaps 13

[illegible]

Db 124 HNGTFEOPVQFRPAHFIHQ-PLPLAD- 153
 Qy 260 SYWNNKPPADSGGKEIFSLPHMADMYMFKGISPAKYSYSPDLPIDQISLKGAA 319
 Db 154 -----VLPLVHPADINTFMVLYQIKTKRLOPFRSLPIDQISLKGAA 198
 Qy 330 FELCQRLNRYFNAETGWECCGLSYCLDPTAG-GFOQLLEPMKFRMYLKLQHEEE 378
 Db 199 VEICHIVNTTFCLOTQNFCLGRLRYIEDGARVGEVELELFFHGTLRKLOQDEE 258
 Qy 379 YLMQALISFSPDRPVQLOHNVQLOEQFATITKSYIEENRQPAHREFLTKAMLE 438
 Db 259 YVLAAMALFSPDRPVQLOHNVQLOEQFATITKSYIEENRQPAHREFLTKAMLE 318
 Qy 439 LRSINAOHTQRLRIODIHPPAPPLMOEL 467
 Db 319 LRSINAEVGYOIHQIGLSAM-WPLQEI 346

RESULT 10

JC4014
 steroid hormone-nuclear receptor NER - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Sep-1999
 C:Accession: JC4014
 R:Shinar, D.M.; Endo, N.; Rutledge, S.J.; Vogel, R.; Rodan, G.A.; Schmidt, A.
 Gene 147, 273-276, 1994
 A:Title: NER, a new member of the gene family encoding the human steroid hormone nuclear
 A:Reference number: JC4014; MID:95011628
 A:Accession: JC4014
 A:Molecule type: mRNA
 A:Residues: 1-461 <SH1>
 A:Cross-references: GB:007132; MID:9641961; PID:AAA61783.1; PID:9641962
 A:Experimental source: osteosarcoma cells SAOS-2/B10
 C:Genetics:
 A:Gene: GDB:UNR
 A:Cross-references: GDB:389570; OMIM:600380
 A:Map position: 19q13.3-19q13.3
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: steroid hormone receptor
 F:85-381/Domain: erba transforming protein homology <ERBA>
 F:87-154/Domain: DNA binding #status predicted <BIN>

Query Match 20.1%; Score 500.5; DB 2; Length 461;
 Best Local Similarity 28.0%; Pred. No. 2e-31;

Matches 134; Conservative 93; Mismatches 153; Indels 99; Gaps 15;

Qy 33 PRGPEANLE-VRPKESMNHADVFHCEDTESVPGKPSVNADEVGPOICRYCGKATGYH 91
 Db 39 PGPRDDVCTDBASACSTDMVTPDEPEPRKKKGPAPMAGHELCTRCVCGKASGFH 98
 Qy 92 ENVMTCGCKGFFRRAMKRNARLRCEFR-KGACETRTTRRQCCARLKLCSGKKEM 150
 Db 99 YNVLSCGCKGFFRRSVYVGARFYACRGCGTCQADATWRRCQCCCRKAKKEMQEC 158
 Qy 151 INSDEAVEBRALLIRKKKEKRGCTQ-PLVQOG- 181
 Db 159 VLSSEGIKKKK--IRKQOQOESOSQSPVQSGSSASPGSGSEASOGSGEGE 216
 Qy 182 ---LVEEQRMIRLMDQMKTFDTFSHFKNFRPLPVLSGCELPESLAPSEAKY 238
 Db 217 GVOLFMAQELMIQQLVAQLOCNKRFS- 252
 Qy 239 SOVRADLCSLKSLQLRGEGSVNWKPPADSGGKEIFSLPHMADMYMFKGISPAK 298
 Db 253 P-----LGAD-----POSRARQORFA--HFTELALISVGEIVDFAK 287
 Qy 299 VLSYFNDLPIDQISLKGAAFEICQLRNTVFNNAETGWECC-GRLSYCLD-TAGG 353
 Db 288 QVPGFLOLRGREDQIALKASTIEIMLTARIRYHET--ECITFLKDFYSKDDFRAG 344

Qy 354 FOQLLEPMKFRMYLKLQHEEYVLMQALISFSPDRPVQLOHNVQLOEQFATITK 413
 Db 345 LQVEFINPIEFSSAMRGLDDDEALALAINIFADRNVOEPGRVALLQOPVEALL 404
 Qy 414 SYIEENRQPAHREFLTKAMLELRSINAOHTQRL-LRIODIHPPAPPLMOELFGI 470
 Db 405 SYTRIKRPOLOLR-FPRMMLKLVSLRTLSVSHSEGVFALRLQD-KKLPLUSEIMDV 459

RESULT 11

A56043
 steroid hormone receptor-like protein RUD-1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 24-Sep-1999
 C:Accession: A56043
 R:Apfel, R.; Benzrock, D.; Lernhardt, E.; Ortiz, M.A.; Salbert, G.; Pfahl, M.
 Mol. Cell. Biol. 14, 7025-7035, 1994
 A:Title: A novel orphan receptor specific for a subset of thyroid hormone-responsive
 A:Reference number: A56043; MID:95021230
 A:Accession: A56043
 A>Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-445 <APE>
 A:Cross-references: GB:U11685; MID:9555751; PID:AAA3633.1; PID:9555752
 A:Note: authors translated the codon GAG for residue 73 as Ser
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: steroid hormone receptor; zinc finger
 F:94-365/Domain: erba transforming protein homology <ERBA>

Query Match 19.9%; Score 496.5; DB 2; Length 445;
 Best Local Similarity 30.1%; Pred. No. 4e-31;

Matches 129; Conservative 84; Mismatches 144; Indels 71; Gaps 13;

Qy 57 EDHESVPGKPSVNADEVGPOICRYCGKATGYHFNVTGCEGCKGFFRRAMKRNARLRC 116
 Db 73 EPELTPORRRKGPAPRMKMGNELCSVCGDKASAFHYNVLSCGCKGFFRRSVIGARYIC 132
 Qy 117 PFRGACETRTTRRQCCARLKLCSGKKEMSDENAEERALLIRKKSE- 170
 Db 133 -HSGGCHPDTMTRKRCQCRRLKCRHAGMECVLSEQIRLKL-LKROEQOAGATS 189
 Qy 171 ---RTGTOPLGVQGLTEQRMIRLMDQMKTFDTFSHFKNFRPLPVLSGCELPESL 227
 Db 190 VSPRVSSPQVLPQLSPEDIGMIKTLVAQQCNRRSS- 228
 Qy 228 QAPSRERAKNVOYKDKCSLKVSLQLRGEGSVNWKPPADSGGKEIFSLPHMADMY 287
 Db 229 ---DRLRYTPW-PIAPD-----POSREARQORFA--HFTELAI 260
 Qy 288 YMFKGISPAKYSYSPDLPIDQISLKGAAFEICQLRNTVFN--AEFTWECGRLSY 345
 Db 261 VSGVEIVPAKLPFLFQDSREDQIALKTSIAIEVMLETSRRINPSESITF-LKDFSY 319
 Qy 346 CLEDTA-GGFOQLLEPMKFRMYLKLQHEEYVLMQALISFSPDRPVQLOHNVQLO 404
 Db 320 NNEEDAKAGLQVEFIWPFERSRSMNELQNDADAFALLIAISFSDRPNVQOOLOVERL 379
 Qy 405 OQOFAITKSYIEENRQPAHREFLTKAMLELRSINAOHTQRL-LRIODIHPPAP 462
 Db 380 QHTVEALHAHAYSVINHP--DRLMFPRLMKLVSLRTLSVSHSEGVFALRLQD-KKLPP 435
 Qy 463 LMQELDEGI 470
 Db 436 ILSEIMDV 443

RESULT 12

I38975
 nuclear orphan receptor LXR-alpha - human
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 20-Sep-1999
 C:Accession: I38975


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Db 7 SLDTPLPENGSPDSTSTSTPTKEEGQENDPPRGSESSSSAYIVLLEDEDEPERKKR 66
QY 69 NADVEVGPQICRVCGDKATGYHFNVTMCEGCKGFFRRAKRNALRCPPR-KGAEIIR 127
Db 67 GPAPLMGHELCRVCGDASGFHNVLVSCGCKGFFRRSYVHAGAGYACRGSGTCOMDA 126
QY 128 KTRQOCACRLRKLCESGCKKEMTMSDAVEERRALIKRKKSERTGQPL- 177
Db 127 FMRRRCQCLRLKCKEAGMREQCYLEEQIRKKRIQKQQQQPPPTPEPSSSARPAAS 186
QY 178 -----GVQGLEBQRMMIRELMDAKMTPTTSSHKNRRLRGVLSGCE 222
Db 187 PGTSEASSQSGEGEGEIO-LTAQELMIQQLVAAQLOCNKRSPS----- 229
QY 223 LPESLQAPSRREAAKWSQVRKDLCSLKVSLQGEDESVWNYKPPADSGKEIFSLPHM 282
Db 230 -----DQKVPWP-----LGAD-----PQSRDARQQAFA--HF 256
QY 283 ADMSTYFKGIISFAKVISYFRDLPIEDQISLLKGAFAELCOLRFTVFNAGTGWEC-- 340
Db 257 TELAIISVOEIVDPKQVPGFLQIGREDQIALKASTIEIMLETARYNHET--ECIT 313
QY 341 --GRLSYCLEP-TAGGFOQLLEPMLKEHYMLKKIOLHEEYVLMQALISLSPDRGVQ 397
Db 314 FLKDFYTKNDPFRAGIQVFEINIFEFRRAMRLGLDDEALALAIIFADHPVQOE 373
QY 398 HRVVDQLQEOFAITLKYISICNRPQAPARFLFLKIMAMLETLSINAQTORL--RIOD 455
Db 374 PSRYEALQCPYVALLSYTRIKRPDQLR--PRMLMKLVSLRTISVSVSEGVFALRIOD 431
QY 456 IHPFAPLMQELFGI 470
Db 432 --KKLPLESEIMDV 444

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RESULT 15

A56918

farnesoid x-activated receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 24-Sep-1999

R:Accession: A56918

R:Forman, B.M.; Goode, E.; Chen, J.; Oro, A.E.; Bradley, D.J.; Perlmann, T.; Noonan, D.J.

Cell 81, 687-695, 1995

A:Title: Identification of a nuclear receptor that is activated by farnesol metabolites.

A:Reference number: A56918; M01D:95292336

A:Accession: A56918

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-469 <FOR>

C:Cross-references: GB:U18374; NID:9868031; PIDN:AAC52205.1; PID:9868032

C:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: DNA binding; nucleus; zinc finger

F1:22-390/Domain: erba transforming protein homology <ERBA>

Query Match 18.6%; Score 463; DB 2; Length 469;

Best local similarity 27.7%; Pred. No. 1.7e-28; Mismatches 161; Indels 110; Gaps 18;

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Db 219 EDSEGRDLRCVSTTKLCREKTELIVDQOTLDYINDYSKO-----RPFQET 267
QY 219 SGCELPESLCAPSRREAAKWSQVRKDLCSLKVSLQGEDESVWNYKPPADSGKEIFSL 278
Db 268 -----NKIKE-----ERSAENFLI 283
QY 279 LPHMADSTYFKGIISFAKVISYFRDLPIEDQISLLKGAFAELCOLRFTVFNAGTGW 338
Db 284 L--TENATSHVOILVEFTKRLPGFQTLDEQIALKSAVEAMFLRSAEIFNKKLPAG 340
QY 339 ECGRLSYCLEP-TAGGFOQLLEPMLKEHYMLKKIOLHEEYVLMQALISLSPDRGVQ 398
Db 341 HADLEERIKS--GISDEYITPMESFYKSGELKTOEYVLAIVLSPDRQYIKR 398
QY 399 RVVDQLQEOFAITLKYISICNRPQAPARFLFLKIMAMLETLSINAQTORL--RIOD 455
Db 399 EAVEKLOEPLDVLQICKIKIYOPENPOH--FACILGRITELRTNHHAMLMKRVND 455
QY 456 IHPFAPLMQELFGI 470
Db 456 -KHF--TPLCEIMDV 468

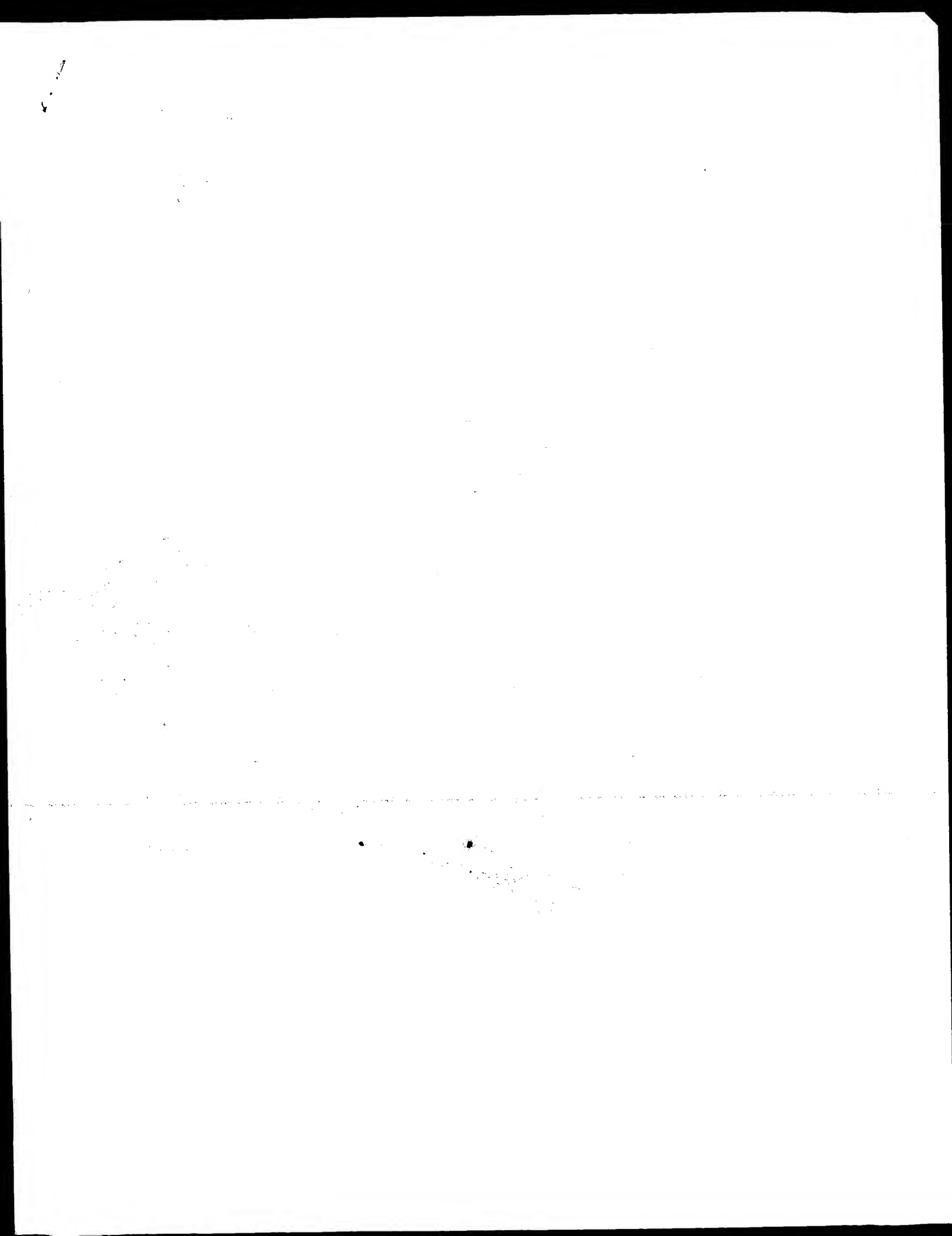
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QY 13 SLRAPAIPLHSAAELASN--HPRGPE-----ANLEVPKESMNADFEVCEDE-- 60
Db 47 NVQFPQVQFOISSSYSLGFTYQPEDWYSPGLYELRRMPTES-----VYGETEVS 100
QY 61 --SYGKPSVNADE--EVGGPQICRVCGDKATGYHFNVTMCEGCKGFFRRAMRNALRC 116
Db 101 EMPVTKRPMAASSAGRKRGDELQVCGDRASGYHYNALTCGCKGFFRRSITFNAYKC 160
QY 117 PERKAGCEITRTKTRQOCACRLRKLCESGCKKEMTMSDAVEERRALIKRKKSERTGTOP 176
Db 161 K-NGNCVMDMYMRKQDCRLRKCKREKMLAECLTEIOCKSKR-LKKNVQHADOQTVN 218
QY 177 LGVQC-----LTEQRMMIRELMDAKMTPTTSSHKNRRLRGVLS 218

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OM protein - protein search, using sw model

Run on: February 18, 2001, 14:31:58 ; Search time 49.49 Seconds
(without alignments)
171.624 Million cell updates/sec

Title: US-09-143-828-4

Perfect score: 2494
Sequence: 1 MYVTRHHEKESLRAFAIP.....QDIHPFAPDLMQELGITGS 473

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_JA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*

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4: /cgn2_6/ptodata/2/1aa/PCUS.COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	768	30.8	348	1	US-08-459-489-10
2	768	30.8	348	1	US-08-458-686-10
3	768	30.8	348	1	US-07-843-350C-10
4	629	25.2	367	1	US-07-737-736B-4
5	500.5	20.1	461	1	US-08-330-518-2
6	500.5	20.1	461	1	US-08-330-283-2
7	500.5	20.1	461	2	US-08-646-248-2
8	500.5	20.1	461	4	PCT-US95-13924-2
9	500.5	20.1	461	4	PCT-US95-13931-2
10	498	20.0	460	1	US-08-342-411A-2
11	491.5	19.7	440	1	US-08-333-358-8
12	491.5	19.7	440	1	US-08-463-684-8
13	491.5	19.7	440	1	US-08-694-501-8
14	491.5	19.7	447	1	US-08-373-935-1
15	490	19.6	446	2	US-08-372-652-3
16	490	19.6	446	2	PCT-US95-16311-3
17	483.5	19.4	443	1	US-08-342-411A-2
18	472.5	18.9	472	1	US-08-496-631-2
19	461	18.5	469	3	US-08-372-183-2
20	461	18.5	469	4	PCT-US95-17023-2
21	452.5	18.1	484	4	US-08-372-652-1
22	452.5	18.1	484	4	PCT-US95-16311-1
23	445	17.8	451	4	US-08-372-652-2
24	445	17.8	451	4	PCT-US95-16311-2
25	432	17.3	355	5	5223606-4
26	428	17.2	348	5	5223606-2
27	424	17.0	746	3	US-09-144-759-18
28	424	17.0	764	3	US-09-144-759-20

29	418	16.8	410	5	5438126-2	Patent No. 5438126
30	414.5	16.6	433	2	US-08-466-120-2	Sequence 2, Appl1
31	414.5	16.6	433	4	PCT-US94-07266-2	Sequence 2, Appl1
32	413	16.6	462	2	US-08-592-383-2	Sequence 2, Appl1
33	413	16.6	462	2	US-08-095-728B-4	Sequence 4, Appl1
34	413	16.6	462	4	PCT-US92-02320A-4	Sequence 4, Appl1
35	413	16.6	797	4	US-08-095-728B-2	Sequence 2, Appl1
36	413	16.6	797	4	PCT-US92-02320A-2	Sequence 2, Appl1
37	409	16.4	368	5	5223606-3	Patent No. 5223606
38	401.5	16.1	403	2	US-08-592-383-4	Sequence 4, Appl1
39	401	16.1	462	5	5171671-2	Patent No. 5171671
40	392.5	15.7	454	5	5260432-2	Patent No. 5260432
41	371	14.9	475	2	US-08-484-200-2	Sequence 2, Appl1
42	371	14.9	475	3	US-08-465-375-2	Sequence 2, Appl1
43	371	14.9	548	1	US-08-333-358-2	Sequence 2, Appl1
44	371	14.9	548	1	US-08-463-694-2	Sequence 2, Appl1
45	371	14.9	548	1	US-08-694-501-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-459-489-10
Sequence 10, Application US/08459489
Patent No. 5686574
GENERAL INFORMATION:
APPLICANT: David D. Moore et al.
TITLE OF INVENTION: CAR RECEPTORS AND RELATED
TITLE OF INVENTION: MOLECULES AND METHODS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSES: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 50z or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,489
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/843,350
FILING DATE: February 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/126001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 348
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: linear
US-08-459-489-10

Query Match 30.8%; Score 768; DB 1; Length 348;

Best Local Similarity 42.2%; Pred. 9.9e-69;

Matches 164; Conservative 62; Mismatches 109; Indels 54; Gaps 6;

QY 80 CRVCGDRTGTHYHNMVTCESCKGFFRRAMKRLRCPFRKACETTRKTRCOACRLR 139

Db 11 CVCGDOATGYHFNALTCGCKGFFRRVTSIGPTCPF-AGSCVSKTORRHCACRLQ 69
 QY 140 KCLESCKMKEMIMSDAVERERALLKRRKSEKGTQPLGVLTEQRMIMRELMDAOK 199
 Db 70 KCLDAGKRMIMLSAVALRRRAKQAQRAQTPVO-----LSKEOELLRTLLGATR 123
 QY 200 TFDTSHEKFNRLPGVLSGCELPESLOAFSREBAKMSQVRKDLCSLKSVALRGDQ 259
 Db 124 HMGTFEQVQPRPAHLFIHQ-PLPTLAP-----153
 QY 260 SWNTKPPADSGKKEIFSLPMDASTYMEKGIISFAKVISYFRDLPIDQISLKGAA 319
 Db 154 -----VLPLVTHFADINTFMVLQVIKFTKDLPVFRSLPIEDQISLKGAA 198
 QY 320 FELCOLRFTVYNAETGWEGRSLCYCLEDTAG-GEOLLLEPMKLFYMKKLOLHEE 378
 Db 199 VEICHTVNTTCLQTONFLCGPLRTTIEDGARVGEFVEFELHFFHGTLRKLOLOPE 258
 QY 379 YVLMQAISLSPDRPGVLQHRVVDLOBOFAITLKSYTECNRPQPAHREPLFKIMAMTE 438
 Db 259 YVLAAMALFSPDRPGVQORDEIDLOQEMALTLQSYIKGOQRPRDRFLYAKLLGLAE 318
 QY 439 LRSINAQHTQRLRIQDIHPATPLMOEL 467
 Db 319 LRSINAYGYQIOHIGLSAM-MPLQEI 346

RESULT 2

US-08-458-686-10
 ; Sequence 10, Application US/08458686
 ; Patent No. 5710017
 ; GENERAL INFORMATION:
 ; APPLICANT: David D. Moore et al.
 ; TITLE OF INVENTION: CAR RECEPTORS AND RELATED
 ; TITLE OF INVENTION: MOLECULES AND METHODS
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 502 or 55SX
 ; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
 ; SOFTWARE: WordPerfect (Version 5.0)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/458,686
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/843,350
 ; FILING DATE: February 26, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul T. Clark
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 00786/126001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 348
 ; TYPE: amino acid
 ; STRANDEDNESS: N/A
 ; TOPOLOGY: linear
 ; US-08-458-686-10

Query Match 30.8%; Score 768; DB 1; Length 348;

Best Local Similarity 42.2%; Pred No. 9,9e-69;
 Matches 164; Conservative 62; Mismatches 109; Indels 54; Gaps 6;
 QY 80 CVCGDKATGYHFNVTTCGCKGFFRRKRNARLCPFRKACETTRRQCCACRLR 139
 Db 11 CVCGDOATGYHFNALTCGCKGFFRRVTSIGPTCPF-AGSCVSKTORRHCACRLQ 69
 QY 140 KCLESCKMKEMIMSDAVERERALLKRRKSEKGTQPLGVLTEQRMIMRELMDAOK 199
 Db 70 KCLDAGKRMIMLSAVALRRRAKQAQRAQTPVO-----LSKEOELLRTLLGATR 123
 QY 200 TFDTSHEKFNRLPGVLSGCELPESLOAFSREBAKMSQVRKDLCSLKSVALRGDQ 259
 Db 124 HMGTFEQVQPRPAHLFIHQ-PLPTLAP-----153
 QY 260 SWNTKPPADSGKKEIFSLPMDASTYMEKGIISFAKVISYFRDLPIDQISLKGAA 319
 Db 154 -----VLPLVTHFADINTFMVLQVIKFTKDLPVFRSLPIEDQISLKGAA 198
 QY 320 FELCOLRFTVYNAETGWEGRSLCYCLEDTAG-GEOLLLEPMKLFYMKKLOLHEE 378
 Db 199 VEICHTVNTTCLQTONFLCGPLRTTIEDGARVGEFVEFELHFFHGTLRKLOLOPE 258
 QY 379 YVLMQAISLSPDRPGVLQHRVVDLOBOFAITLKSYTECNRPQPAHREPLFKIMAMTE 438
 Db 259 YVLAAMALFSPDRPGVQORDEIDLOQEMALTLQSYIKGOQRPRDRFLYAKLLGLAE 318
 QY 439 LRSINAQHTQRLRIQDIHPATPLMOEL 467
 Db 319 LRSINAYGYQIOHIGLSAM-MPLQEI 346

RESULT 3

US-07-843-350C-10
 ; Sequence 10, Application US/07843350C
 ; Patent No. 5756448
 ; GENERAL INFORMATION:
 ; APPLICANT: David D. Moore et al.
 ; TITLE OF INVENTION: CAR RECEPTORS AND RELATED
 ; TITLE OF INVENTION: MOLECULES AND METHODS
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 502 or 55SX
 ; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
 ; SOFTWARE: WordPerfect (Version 5.0)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/843,350C
 ; FILING DATE: February 26, 1992
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul T. Clark
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 00786/126001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 348
 ; TYPE: amino acid
 ; STRANDEDNESS: N/A

TOPOLOGY: linear
US-07-843-350C-10

Query Match 30.8%; Score 768; DB 1; Length 348;
Best Local Similarity 42.2%; Pred. No. 9,9e-69;
Matches 164; Conservative 62; Mismatches 109; Indels 54; Gaps 6;

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DB 11 CVCCKATGATGHNFMVTECGCGKGFRRAMKRNARLRCFRRKAGACETRRKROCOACRLR 69
QY 140 KLESGMKKEKMSDEAVERRALIKKKEKERTGTPLOVGGITTEGQRMVIRELDAQMK 199
DB 70 KCLAGMKRMDLSAEMALARRAKOARRAQGPVQ-----LSKQBELIRLGAHR 123
QY 200 TFDTFSEFKRRLPGVLSGCEPESLOAPSEBAKMSQVKKDCSLKVSLOLNGEGG 259
DB 124 HMGTFEFGVFRPPLFIHQ-PLFTLP----- 153
QY 260 SWNYKPPADSGKEIFSLPHNADSTYMKGIISFAKISYFRDLPIDQISLKGAA 319
DB 154 -----VLPYTHFADINTFVQLVKTNDLPFRSLPIEDQISLKGAA 198
QY 320 FELQALFNTVFNATETGECGRSLCYETAG-GRQQLLEPMLKFRYMKKLOLHEE 378
DB 199 VEIHYLVNTEFCLOTQNFCLGRLRTIEDGAVGQVEFLLELFFHGTLRKLOPE 258
QY 379 VYLMQALSTSPDRPGVQLHRRVDOLOEOPATLKSYIECNRPQARHRELFKIMAMLE 438
DB 259 VYLLAVALSPDRPGVQTOGDEIDQLOEEMALLOSITINGQRRPDRNLYMLGLAE 318
QY 439 LRSINAOHTORLRIODIHPFATPLMOEL 467
DB 319 LRSINAEYGYOIHQIGLSAM-MPLQEI 346

RESULT 4
US-07-737-736B-4

Sequence 4, Application US/07737736B
Patent No. 5260199

GENERAL INFORMATION:

APPLICANT: Deluca, Hector F.

APPLICANT: Ross, Troy K.

APPLICANT: Prael, Jean M.

TITLE OF INVENTION: Method Of Producing

NUMBER OF SEQUENCES: 1,25-Dihydroxyvitamin D3 Receptor Protein

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carl R. Schwartz, Esq., c/o Quarles & Brady

STREET: 411 East Wisconsin Avenue

CITY: Milwaukee

STATE: Wisconsin

COUNTRY: U.S.A.

ZIP: 53202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/737,736B

FILING DATE: 19910730

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Schwartz, Carl R.

REGISTRATION NUMBER: 29,437

REFERENCE/DOCKET NUMBER: 96-296-2185-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 414-277-5715

TELEFAX: 414-277-5774

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 367 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rat
PUBLICATION INFORMATION:
AUTHORS: Burmeister, James K.
AUTHORS: Maeda, No. 5260199yo
AUTHORS: Deluca, Hector F.
TITLE: Isolation and expression of rat
TITLE: 1,25-dihydroxyvitamin D3 receptor cDNA
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 85
PAGES: 1005-1009
DATE: February-1988
US-07-737-736B-4

Query Match 25.2%; Score 629; DB 1; Length 367;
Best Local Similarity 38.5%; Pred. No. 8.7e-55;
Matches 144; Conservative 70; Mismatches 132; Indels 28; Gaps 9;

QY 113 RLCPFRKAGCEITRRTRKROCOACRLKCLSGMKKEMISDEAVERRALIKRKSERT 172
DB 1 RLCFPR-NGCRITKRNRRHCOACRLKRCVDIGMKKEFLTDEYQRRKEMIKRKEEA 59
QY 173 GTPLGVQGLTEFORAMIRELDAQMKTEPDTFSFKNRLPGV--SSGCELPESLOAP 230
DB 60 LKDSLRK-LSERQCHITILDAHKKITDPTVADFRPFRVRRDGGTSYSR---P 114
QY 231 SREBAKMSQVRRDLCSLKY-----SLQNGEDGSVNYKPPADSGKEIFSLPH 281
DB 115 TLFSGNSSSSSDLYTTSIDMWERPSSNLDNGEDS----DPSTYTLDSPLSHPH 169
QY 282 MADSTYMKGIISFAKISYFRDLPIDQISLKGAAPELQALFNTVFNATETGECG 341
DB 170 LADLVSTIGKVIYGRKMLPGFRDLTSDQIYTLKSSAIEVIMKRSNOSFTMDMSDCG 229
QY 342 RLSCLEDT---AGFQOQLLEPMLKFRYMKKLOLHEEVLMOALSTSPDRPGVQLH 398
DB 230 SODKYKDVTVSKAGHTLELEPLIKFQVGLKNTLHEEVLMACTVSPDRPGVQDA 289
QY 399 RYVDOLOEOPATLKSYIECNRPQARHRELFKIMAMLELRSINAOHTQ--RLRIQDI 456
DB 290 KIVEAIODRLSNTQTYTRCRHPPGSHQLYAKMIQKLAJLRLSINEBSKQYRSLSQPE 349
QY 457 HPF-ATPLMOELFG 469
DB 350 NSMKLPLVLEVFG 363

RESULT 5

US-08-330-518-2

Sequence 2, Application US/08330518

Patent No. 5607967

GENERAL INFORMATION:

APPLICANT: Friedman, Eitan

APPLICANT: Holloway, M. Katharine

APPLICANT: Rodan, Gideon

APPLICANT: Schmidt, Azriel

APPLICANT: Vogel, Robert

TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 East Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: US

OY 414 SYIECNROPAPHRFLFKIMAMTELRSINAOHTORL--LRIODIHPATPLMOELFGI 470
 DB 405 SYTRIKRPQDQRL--FPRMLKLVSLRTLSVSHSEOVFALRIOD--KRLPILSEIMDV 459

RESULT 7

US-08-646-248-2
 ; Sequence 2, Application US/08646248
 ; Patent No. 593932
 ; GENERAL INFORMATION:
 ; APPLICANT: Friedman, Eitan
 ; APPLICANT: Holloway, M. Katharine
 ; APPLICANT: Rodan, Gideon
 ; APPLICANT: Rutledge, Su Jane
 ; APPLICANT: Schmidt, Azriel
 ; APPLICANT: Vogel, Robert
 ; TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merck & Co., Inc.
 ; STREET: 126 East Lincoln Avenue
 ; CITY: Rahway
 ; STATE: New Jersey
 ; COUNTRY: US
 ; ZIP: 07065-0907
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/646,248
 ; FILING DATE: 14-MAY-1996
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/230,283
 ; FILING DATE: 27-OCT-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dolan, Catherine A.
 ; REGISTRATION NUMBER: 36,502
 ; REFERENCE/DOCKET NUMBER: 19327
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 594-4283
 ; TELEFAX: (908) 594-4720
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 461 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-646-248-2

Query Match 20.1%; Score 500.5; DB 2; Length 461;
 Best Local Similarity 28.0%; Pred. No. 8.9e-42;
 Matches 134; Conservative 93; Mismatches 153; Indels 99; Gaps 15;

OY 33 PRGPANLE-VPRKESMNADFYHCEDTESVPGKPSVNADEEVGPOICRVCGDKATGYH 91
 DB 39 PGGPDPVPGTDEASASTVDIPDPPEEPERKRRKGPAPKMLGHELCRYCGDKASGFH 98
 OY 92 FVMTCEGCKGFERAMRNALRCFPR-KGACETTRKTRBQCAQCRKKGESGMKREM 150
 DB 99 YNVLSCGCKGFERRSVVGARATACGGGTCQADATMRKCCQCRURKCKEAGMREQC 158
 OY 151 IMSDAVERRALIRKKSERTGTQ---PLGVQG----- 181
 DB 159 VLSEQDIKKR--IRKQGOSESQSQSPVYGQSSSSASASPGSGSAGSGSGGGE 216
 OY 162 ---LTEBORAMIRELMDAMQKTTDTTFSHFNKRLPGVLSSGCELPESLQAPSRBAKW 238

DB 217 GVOITAAQELMTIOOLVAADQCKRSFS-----DQPRVTPW 252
 OY 239 SOVRKDCSLKVLQLRGEGESVWNNKPPADSGCKFIISLPLPMADMSTYKFGIISFAK 298
 DB 253 P-----LGAD-----POSRAQORFA---HTELATISVOEIVDFAK 287
 OY 299 VISYFRDPLIEDOISLKGAFELCOLRENTVYNAETGTWEC---GRLSYLED-TAGC 353
 DB 288 QVPGFLQIGREDQIALKASTIEMLETARRYNHE-----ECTFLKDTYKDKDFHRAG 344
 OY 354 FQOLLEPMKFTYMLKQLQHEEYVLMQAISLSESPDPRVQLQHRVDQLQOPATYTK 413
 DB 345 LOVEFNPIEFESRAMRRLGLDAEYALLAINIFSADRPVQEPGRVVALQOPYEALL 404
 OY 414 SYIECNROPAPHRFLFKIMAMTELRSINAOHTORL--LRIODIHPATPLMOELFGI 470
 DB 405 SYTRIKRPQDQRL--FPRMLKLVSLRTLSVSHSEOVFALRIOD--KRLPILSEIMDV 459

RESULT 8

PCT-US95-13924-2
 ; Sequence 2, Application PC/TUS9513924
 ; GENERAL INFORMATION:
 ; APPLICANT: Friedman, Eitan
 ; APPLICANT: Holloway, M. Katharine
 ; APPLICANT: Rodan, Gideon
 ; APPLICANT: Rutledge, Su Jane
 ; APPLICANT: Schmidt, Azriel
 ; APPLICANT: Vogel, Robert
 ; TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merck & Co., Inc.
 ; STREET: 126 East Lincoln Avenue
 ; CITY: Rahway
 ; STATE: New Jersey
 ; COUNTRY: US
 ; ZIP: 07065-0907
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/13924
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Quagliato, Carol S.
 ; REGISTRATION NUMBER: 35,330
 ; REFERENCE/DOCKET NUMBER: 19327 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 594-3809
 ; TELEFAX: (908) 594-4720
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 461 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; PCT-US95-13924-2

Query Match 20.1%; Score 500.5; DB 4; Length 461;
 Best Local Similarity 28.0%; Pred. No. 8.9e-42;
 Matches 134; Conservative 93; Mismatches 153; Indels 99; Gaps 15;
 OY 33 PRGPANLE-VPRKESMNADFYHCEDTESVPGKPSVNADEEVGPOICRVCGDKATGYH 91

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Db 39 PGFPDPVPGTDEASASCTDWTVPDPEEPERKKKGPAPKMLGHELCHVCGDKASGFH 98
QY 92 FNVMTCEGCKGFFRRARNRNALRCPPR-KGACEITRTKTRQOACRLKCSGKMKEM 150
Db 99 YNVLSCEGCKGFFRRSVRGARACRGGGTCQMDAPMRKCCQCLRKCKEAGMRBQC 158
QY 151 IMSDEAVERBALIRKKKSERTGTQ---PLGVQO-----181
Db 159 VLSEEDIRKKK--IRKQOQESQSQSPVPGQSSSSASPGASPGSGSAGSGSGE 216
QY 182 ---LTEROQRMIRELMDQAKMTFDTFSHFKNRPLPGVLSGCELPESLOAPSRBEAKW 238
Db 217 GVQLTAAQELMIOQLVAQLOCNKRSFS-----DQPKVTPW 252
QY 239 SQVRKDCSLKVSQLRGEGSVNNYKPPADSGKEIFSLPHMADSTYFKGIIISFAK 298
Db 253 P-----LGAD-----POSDARQORFA--HFTELAIISVQEIYDFAK 287
QY 299 VISYFRDLPIDQISLKGAFELCOLRNFVNAETGTWEC---GLSTCYLED-TAGC 353
Db 288 QVPGFLQGRDQIALKASTIEIMLETARVNHET--BCITFLKDFYTSKDFHRAG 344
QY 354 FOQLLEPMLKFFHYMLKKQLQHEEYVLMQALISLSPDRPGVLQHRVVDLOEQFAITLK 413
Db 345 LOVEFINPIFFESRMRRLGIDDAEYALILAINIFSADRPVQEGRVEALQOQPYVEALL 404
QY 414 SYIECNRQPARHFLFKIMAMTELRSINQHTQRL--LRIDIHFPATPLMOELFCI 470
Db 405 SYTRIKRPQDQLR--FPRMLKMLVSLRITLSSVSHSQVYALRLQD--KKPLPLSEIMDV 459

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RESULT 9

PCT-US95-13931-2

Sequence 2, Application PC/TUS9513931

GENERAL INFORMATION:

APPLICANT: Friedman, Eitan

APPLICANT: Holloway, M. Katharine

APPLICANT: Rodan, Gideon

APPLICANT: Schmidt, Azriel

APPLICANT: Vogel, Robert

TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 East Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: US

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13931

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Quagliato, Carol S.

REGISTRATION NUMBER: 35,330

REFERENCE/DOCKET NUMBER: 19316 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3809

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 461 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO
PCT-US95-13931-2

Query Match 20.1%, Score 500.5; DB 4; Length 461;
Best Local Similarity 28.0%; Pred. No. 8.9e-42;
Matches 134; Conservative 93; Mismatches 153; Indels 99; Gaps 15;

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QY 33 PRGPEANLE-YPRKSNMHADEFHCEDESVYGRKSVNADSEGPCQICRYGDKATGYH 91
Db 39 PGFPDPVPGTDEASASCTDWTVPDPEEPERKKKGPAPKMLGHELCHVCGDKASGFH 98
QY 92 FNVMTCEGCKGFFRRARNRNALRCPPR-KGACEITRTKTRQOACRLKCSGKMKEM 150
Db 99 YNVLSCEGCKGFFRRSVRGARACRGGGTCQMDAPMRKCCQCLRKCKEAGMRBQC 158
QY 151 IMSDEAVERBALIRKKKSERTGTQ---PLGVQO-----181
Db 159 VLSEEDIRKKK--IRKQOQESQSQSPVPGQSSSSASPGASPGSGSAGSGSGE 216
QY 182 ---LTEROQRMIRELMDQAKMTFDTFSHFKNRPLPGVLSGCELPESLOAPSRBEAKW 238
Db 217 GVQLTAAQELMIOQLVAQLOCNKRSFS-----DQPKVTPW 252
QY 239 SQVRKDCSLKVSQLRGEGSVNNYKPPADSGKEIFSLPHMADSTYFKGIIISFAK 298
Db 253 P-----LGAD-----POSDARQORFA--HFTELAIISVQEIYDFAK 287
QY 299 VISYFRDLPIDQISLKGAFELCOLRNFVNAETGTWEC---GLSTCYLED-TAGC 353
Db 288 QVPGFLQGRDQIALKASTIEIMLETARVNHET--BCITFLKDFYTSKDFHRAG 344
QY 354 FOQLLEPMLKFFHYMLKKQLQHEEYVLMQALISLSPDRPGVLQHRVVDLOEQFAITLK 413
Db 345 LOVEFINPIFFESRMRRLGIDDAEYALILAINIFSADRPVQEGRVEALQOQPYVEALL 404
QY 414 SYIECNRQPARHFLFKIMAMTELRSINQHTQRL--LRIDIHFPATPLMOELFCI 470
Db 405 SYTRIKRPQDQLR--FPRMLKMLVSLRITLSSVSHSQVYALRLQD--KKPLPLSEIMDV 459

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RESULT 10

US-08-342-411A-2

Sequence 2, Application US/08342411A

Patent No. 5639616

GENERAL INFORMATION:

APPLICANT: LIAO, Shutsung

APPLICANT: SONG, Ching

TITLE OF INVENTION: UNIDENTIFIED NUCLEAR RECEPTOR

TITLE OF INVENTION: COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/342,411A

FILING DATE: 18-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KITCHELL, BARBARA S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: ARCD154

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679
 TELE: 79-0924
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 460 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-342-411A-2

Query Match 20.0%; Score 498; DB 1; Length 460;
 Best Local Similarity 27.4%; Pred. No. 1.6e-41;
 Matches 143; Conservative 87; Mismatches 134; Indels 138; Gaps 18;

20 PLHSAALASLHNPGRPEANLEVRKRESWNHADFHCEDTESVPG--KPSVNADEEVG-- 75
 4 PPSLDTPLRGCGPPQPCA-----PSSS-----PTVKEEGEPWPGGPPDPVGTDEASSA 54
 76 -----GPOICVCGDKATGTHNVMTCEGCKGFFRRAM 108
 55 CSTDWIIPDEEPEPERKKRKGAPRMGLCHELCVCGRKASGFHYNYVLDCGCKGFFRRSV 114
 109 KNNARLRCPFR-KGACEITRTRRQOCRLKCLSGKKKMMINSDEAVEERRALLIRK 167
 115 VGGARRVACRGCGTCQMDAFMRRCQOCRLKCKEAGREGCVLSEQIRKK--IRKQ 172
 168 KSERTGTQ---PLGVQ-----LLEQRMIRELMD 195
 173 QQQQSQSQSQSVPGQSSSSASGPGASPGSEASQSGEGEVQLTRNAQELMQLVYA 232
 196 AQMTFTDTTFSHFKNRFLPGVLSGCELPESIQADPSREBAKWSQVRKDLCSLKVQLQR 255
 233 AOLQCNKRFS-----DQPTVTPW-----L 253
 256 GEDGSVWNNKPPADSGKREIFSLPHMADNMYMFKGIISFAKVISYRDLPIEDQISL 315
 254 GAD-----PQSRDARQORFA--HFTELAIISVOEIVDFAKQVGGVQLGRREQIALL 303
 316 KGAPELCLQRTNVTNFMETGTWEC---GRLSYCLEL-TAGGFQOLLLEPMKAFHLLK 370
 304 KASTIEIMLETARVYNNHET---ECITFLKDTYSKDDPHRAGLQVEITNPIFEESKMR 360
 371 KQQLHEEYVLMQAIISLSPDRPGVQLQHRVDOLOEQFAITLKSTIECNRPQPAHRLFL 430
 361 RGLGDAEYALLAIINIFESADRPVQEPGRVHALQAPYEALLSYTRKRRQDQRR--FP 418
 431 KIMAMTELRSINQHTORL--LRIDQIHPRFATPLMQLFGI 470
 419 RMLMKLVSLRTLSSVHSEGVFALRLQD--KKLPILLSEIMDV 458

RESULT 11
 US-08-333-358-8
 Sequence 8, Application US/0833358
 Patent No. 5571696
 GENERAL INFORMATION:
 APPLICANT: EVANS Ph.D., RONALD M.
 APPLICANT: MANGELSDORF Ph.D., DAVID J.
 APPLICANT: ONG MS., ESTELITA S.
 APPLICANT: ORO Ph.D., ANTHONY E.
 APPLICANT: BORGMEYER Ph.D., UWE K.
 APPLICANT: GIGDERE Ph.D., VINCENT NMN
 APPLICANT: YAO Mr., TSO-PANG NMN
 TITLE OF INVENTION: NOVEL RECEPTORS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Preity, Schroeder, Brueggemann & Clark
 STREET: 444 So. Flower St., Suite 2000
 CITY: Los Angeles
 STATE: CA
 COUNTRY: US
 ZIP: 90071-2921
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentia Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/333,358
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/761,068
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Reltex Ph.D., Stephen E.
 REGISTRATION NUMBER: 31192
 REFERENCE/DOCKET NUMBER: P31 8936
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 440 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-333-358-8

Query Match 19.7%; Score 491.5; DB 1; Length 440;
 Best Local Similarity 29.7%; Pred. No. 6.6e-41;
 Matches 127; Conservative 85; Mismatches 145; Indels 71; Gaps 12;

57 EDIESVPGKPSVNADEEVGPGQICRVGDKATGTHNVMTCEGCKGFFRRAMRNRLNC 116
 68 EPTEIRPQKRKKGPAPRMGLNCLCSVCGDASGFHYNYVLSCGCKGFFRRSVKGNHYIC 127
 117 PFRKGACEITRTRRQOCRLKCLSGKKKMMINSDEAVEERRALLIRKSE----- 170
 128 -HSGGHCPRMDTYMRRKQCECRRLKRCQAGRECVLSEQIRLKK--LRQEEQAHATS 184
 171 ---RTGQPIGVGGLTEEQMMIRELMDQMKTFDTTFSHFKNRFLPGVLSGCELPESL 227
 185 LPPRRSPQILPOLSPESQAGMLEKLVAAQOCNRRSFS----- 223
 228 QASREBAKWSQVRKDLCSLKVSLQLRGEDGSVWNNKPPADSGKREIFSLPHMADNMT 287
 224 ---DLRLVTPWPAW-----DPSRAKQORFA--HFTELAI 255
 288 YMRGIISFAKVISYRDLPIEDQISLKGAEELCOLRENTVFN--AETGTWECGRLSY 345
 256 VSVQEIYDFAKQLPGLQLSREDOIALKTSALIEVMLLETSTRYNGSSSYTF-LKDFSY 314
 346 CLEDTA-GGFQOLLLEPMKAFHMLKKQLHEEYVLMQAIISLSPDRPGVQLQHRVDOLO 404
 315 NREDFPAAAGLQVEITNPIFEESRANMELQNDAEFLLAISIFSDRPNVDOQLVERL 374
 405 QEQFAITLKSYICNRPQPAHRLFLKIMAMTELRSINQHTORL--LRIDQIHPRFAP 462
 375 QHYVEVLAHYVGINHPH--DLRLFPRMLKLVSLRTLSSVHSEGVFALRLQD--KKLP 430
 463 LMQELFGI 470
 431 LLSIEMDV 438

RESULT 12
 US-08-463-694-8
 Sequence 8, Application US/08463694
 Patent No. 5696233
 GENERAL INFORMATION:
 APPLICANT: EVANS Ph.D., RONALD M.
 APPLICANT: MANGELSDORF Ph.D., DAVID J.
 APPLICANT: ONG MS., ESTELITA S.
 APPLICANT: ORO Ph.D., ANTHONY E.

```

APPLICANT: BORGMEYER Ph.D., UWE K.
APPLICANT: GIGUERE Ph.D., VINCENT NMN
APPLICANT: YAO M., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,694
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/761,068
FILING DATE: 17-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8936
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-694-8

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Query Match 19.7%; Score 491.5; DB 1; Length 440;
Best Local Similarity 29.7%; Pred. No. 6.6e-41;
Matches 127; Conservative 85; Mismatches 145; Indels 71; Gaps 12;

QY 57 EDTESVPGKPSVNADEEVGGPOICRYCGDKATGYHFNWTCGCGCGFFRRAMKRNALRC 116
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
Db 68 EPTLRPQKRRKGPAPKMLGNELCSVCGDKASGFHYNYLSCGCGFFRRSVIKGAHYIC 127
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
QY 117 PFRKACEITRTRROCOACRLKCLSGMKEMIMSDAEVERRALIKRKSE----- 170
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
Db 128 -HSGGHCMDTYMRKRCQCRKRCQAGRECVLSEQIRLKK--LKRDEEQAHTS 184
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
QY 171 ---RTGTOPLGVOGLTEORMMIRELMDAOMKTFTDTSFHKNFRLPGVLSGCELPESL 227
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
Db 185 LPPRRSSPPQIILPOLSPBLGMIEKLVAQAQCCNRKRS----- 223
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
QY 228 QAPSRREAAKWSQVRKDCSLKVSQLRGDEGSVWNYPPADSGCKEITFSLPHMADMT 287
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
Db 224 ---DLRATVPMPAD-----DPSREARQAQFA---HFTELAI 255
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
QY 288 YMFKGIIISFAVITYFRDPIEDQISLKGAFELCOLRFTVFN--AETGTWECGRISY 345
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
Db 286 VSYQGIIVDFAPQQLPGLSLRSDQIALKTSAIEVMLETSTRYNPGESEITF-LKDFSY 314
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
QY 346 CLEDTA--GGFOQLLEPMKTRHYMLKQJLHEEYVLMQAISLSPDPFGVLOHRYVDOL 404
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
Db 315 NREPFAPKGLQVEFINPFESRAMNELQDLNDAEFALLAISIPSADPNVODQLQVERL 374
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
QY 405 QEOFAITLKYTECNRPPARHFLFLKIMAMTELRSINAQHTQRL--LRIDQIHPRATP 462
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
Db 375 QHTYBALHAYVSIHHP--DLRMFPRMLAKVSLKTLISVHSGQVRLKLD--KLHP 430
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
QY 463 LMQELFGI 470
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |

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Db 431 LTSEIMDV 438
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
RESULT 13
US-08-694-501-8
; Sequence 8, Application US/08694501
; Patent No. 5710004
; GENERAL INFORMATION:
APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONG M.S., ESTELITA S.
APPLICANT: ONG Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., UWE K.
APPLICANT: GIGUERE Ph.D., VINCENT NMN
APPLICANT: YAO M., TSO-PANG NMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,501
FILING DATE: 07-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/333,358
FILING DATE:
APPLICATION NUMBER: US/07/761,068
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8936
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-694-501-8

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Query Match 19.7%; Score 491.5; DB 1; Length 440;
Best Local Similarity 29.7%; Pred. No. 6.6e-41;
Matches 127; Conservative 85; Mismatches 145; Indels 71; Gaps 12;

QY 57 EDTESVPGKPSVNADEEVGGPOICRYCGDKATGYHFNWTCGCGCGFFRRAMKRNALRC 116
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
Db 68 EPTLRPQKRRKGPAPKMLGNELCSVCGDKASGFHYNYLSCGCGFFRRSVIKGAHYIC 127
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
QY 117 PFRKACEITRTRROCOACRLKCLSGMKEMIMSDAEVERRALIKRKSE----- 170
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
Db 128 -HSGGHCMDTYMRKRCQCRKRCQAGRECVLSEQIRLKK--LKRDEEQAHTS 184
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
QY 171 ---RTGTOPLGVOGLTEORMMIRELMDAOMKTFTDTSFHKNFRLPGVLSGCELPESL 227
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
Db 185 LPPRRSSPPQIILPOLSPBLGMIEKLVAQAQCCNRKRS----- 223
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |
QY 228 QAPSRREAAKWSQVRKDCSLKVSQLRGDEGSVWNYPPADSGCKEITFSLPHMADMT 287
| | | | | : : : | : | | | | : | : | | | | | | | | | | | | | | | | |

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Db 224 ---DRLRTVTPWMPAP-----DPHSRBAQORFA---HTELAI 255
QY 288 YMEGLISFAKVISYFEDLPIDQISLKGAEELCOLRENTVEN--AETGTWECGRLSY 345
Db 256 VSVQEIYDAFAKQLPGFQLSREDQIALKTSAIEVMLTSRNYNGSSSITF-LKDFSY 314
QY 346 CLEDTA-GGFOQLLEPMLEKHYMLKLOLHEEYVLMQALISFSPDRPGVLOHRYVDOL 404
Db 315 NREDFAKAGLOVERINFIFESFRANMELQINDAEFALLAISIFSDRPNVDOLQOVERL 374
QY 405 QEQFATLTKSYIECNRPQAPARHFLKIMAMLETLSINAQHTORL--LRIDIHFPATP 462
Db 375 QHTVEALHNAVYSIHHPH--DRLMFPMLMKLVSLRTISSVSEOVFALRLQD--KKLP 430
QY 463 LMDELGI 470
Db 431 LLEIMDV 438

RESULT 14
US-08-373-935-1
Sequence 1, Application US/08373935
Patent No. 5747661
GENERAL INFORMATION:
APPLICANT: Evans, Ronald M.
APPLICANT: Mangelsdorf, David J.
TITLE OF INVENTION: IDENTIFICATION OF A DISTINCT
TITLE OF INVENTION: RETINOID-RESPONSIVE PATHWAY AND USES THEREFOR
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373.935
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9894
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-4737

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-373-935-1

Query Match 19.7%; Score 491.5; DB 1; Length 447;
Best Local Similarity 29.7%; Pred. No. 6.7e-41;
Matches 127; Conservative 85; Mismatches 145; Indels 71; Gaps 12;

QY 57 EDTESVPGKPSVNADEVGGPOICVCDKATGYHFNMTCEGCGFFRRAMKRNALRLC 116
Db 75 EPTETIRPQRRKGPAPKMLGKLGELSCVCDKASGFHYNTLSCGCKGFFRSVIGKAHYIC 134
QY 117 PRRKAGCEITRTKROCCACRLKCLSGAKKEMINSDEAVEERALLIKRKE-----170
Db 135 -HSGCHCPMDIYMRKRCQECRLRCRQAGMRCEVLSSEQIRLTK--LKRQEEQAHATS 191

QY 171 ---RTGTOPIGVGLTEQRMREINDAQMKTFTDTSHEKNERLPGLVSSGCELPESL 227
Db 192 LPPRRSSPPTILPOLSPEDQGMTEKLVAAQQCNRRSF-----230
QY 228 QAPSREBAWMSQVRDLCSLKVSLQLRGEGDSVNNYKRPADSGKEIFSLPHADNST 287
Db 231 ---DRLRTVTPWMPAP-----DPHSRBAQORFA---HTELAI 262
QY 288 YMEGLISFAKVISYFEDLPIDQISLKGAEELCOLRENTVEN--AETGTWECGRLSY 345
Db 263 VSVQEIYDAFAKQLPGFQLSREDQIALKTSAIEVMLTSRNYNGSSSITF-LKDFSY 321
QY 346 CLEDTA-GGFOQLLEPMLEKHYMLKLOLHEEYVLMQALISFSPDRPGVLOHRYVDOL 404
Db 322 NREDFAKAGLOVERINFIFESFRANMELQINDAEFALLAISIFSDRPNVDOLQOVERL 381
QY 405 QEQFATLTKSYIECNRPQAPARHFLKIMAMLETLSINAQHTORL--LRIDIHFPATP 462
Db 382 QHTVEALHNAVYSIHHPH--DRLMFPMLMKLVSLRTISSVSEOVFALRLQD--KKLP 437
QY 463 LMDELGI 470
Db 438 LLEIMDV 445

RESULT 15
US-08-372-652-3
Sequence 3, Application US/08372652
Patent No. 5932699
GENERAL INFORMATION:
APPLICANT: Moore, David
APPLICANT: Secl, Wongl.
APPLICANT: Chcl, Heng-Sik
TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372.652
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/246001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
Telex: 200154

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-372-652-3

Query Match 19.6%; Score 490; DB 2; Length 446;
Best Local Similarity 29.1%; Pred. No. 9.5e-41;
Matches 125; Conservative 84; Mismatches 128; Indels 92; Gaps 14;

Tue Feb 20 09:10:30 2001

us-09-143-828-4.rai

Page 10

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OY 76 GPQICRCVCGKATGYHHNNWNTCEGCGFFERRAKRNANLRCPPR--KGAEITRKTROCO 134
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
Db 74 GHELCRCVCGDASGFPHNVLTSCBCKGFERRSVYHGAGHACRGSCTCOMAFMRKCO 133
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
OY 135 ACRLRCLCSGEMKEMIMDSAEVAFERALLIRKKSER-----TGTOP 176
   |||||+-----+-----+-----+-----+-----+-----+-----+-----+-----+
Db 134 LCRLRCLCSGEMARQCVLSREQIRKKR--I0K00000PPPESEPAASSSGRPAASPTSE 191
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+
OY 177 LGVG-----LTEGRNATIRFLMOAKMTPTTSHKRNRLRGVLSGGELPESLO 228
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+
Db 192 ASSQSGEGEIOITLFAOELMIOQLVAAQLOCNKRSFS----- 229
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+
OY 229 APSREAKMGSQVRDLCSLKVSLQNGEDGSVNNYPPADSGKELTSLPHMADMTY 288
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+
Db 230 --DQKVPMP-----LGAD-----POSBDANQGRFA--HFTELATI 262
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+
OY 289 MFKGIISPAKVIISYFRDLPIEDQISLKGAFELCOLRNTVFAEIGTWEC-----GRLS 344
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+
Db 263 SVOEIVDPAKOVPGFLQGRDIOALLKASTIETMLQTAIRVNHET--ECITFLKDFI 319
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+
OY 345 YCLSD--TAGGFOQLLEPMLKFHWLKKTLQTHHEEYVLMOAI SLFSDRGVLOHRYVDO 403
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+
Db 320 YSKDFFHRAGLOVEINIFEFSSAMRLGDGDAEYVALLAINFSDRBNVOEPSRYEA 379
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+
OY 404 LOEFOATILKSYIECNRPOPAHRFLFLKIMAMTELBSINAOHQRL--LRIDIHFEAT 461
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+
Db 380 LOOPVEALMLSTRIKRPODLR--FPRMLKMLVSLTLSSVSHSEYFAALRLOD--KKLP 435
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+
OY 462 PLMOELFGI 470
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+
Db 436 PLUSETMDV 444
   +-----+-----+-----+-----+-----+-----+-----+-----+-----+

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Search completed: February 18, 2001, 14:31:59
Job time: 6202 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2001, 14:29:39 ; Search time 63.99 seconds

(without alignments)
252.753 Million cell updates/sec

Title: US-09-143-828-4

Perfect score: 2494

Sequence: 1 MVTYRTNHFKEGSLRAFAIP.....ODIHPPATPLMQLFGITGS 473

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_2/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /cgn2_2/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /cgn2_2/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /cgn2_2/gcgdata/geneseq/geneseq/AA1983.DAT.*
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12: /cgn2_2/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /cgn2_2/gcgdata/geneseq/geneseq/AA1992.DAT.*
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21: /cgn2_2/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2494	100.0	473	20	Y25411 Human nmr7-1 prote
2	2494	100.0	473	20	Y15936 A human intranucle
3	2494	100.0	473	20	Y15933 A human intranucle
4	2494	100.0	473	20	Y09516 Human vitamin D re
5	2334	93.6	457	20	Y16035 A human intranucle
6	2334	93.6	457	20	Y15932 A human intranucle
7	2334	93.6	457	20	Y25410 Human nmr7 partial
8	2289	91.8	434	20	Y15931 A human intranucle
9	2287	91.7	437	20	Y09515 Human vitamin D re
10	2171	87.0	434	20	Y21799 Human steroid and
11	2167	86.9	414	20	Y42691 Human pregnane X r
12	1585	63.6	316	20	Y42689 H186-pregnane X r

13	979.5	39.3	386	17	R98521 Xenopus orphan rec
14	801	32.1	423	20	W94523 Rat vitamin D rece
15	798	32.0	423	19	W47509 Rat vitamin D rece
16	791	31.7	427	20	Y09035 Human vitamin D re
17	789	31.6	427	19	W68156 Human vitamin D re
18	789	31.6	427	20	Y09054 Human vitamin D re
19	789	31.6	427	20	Y09056 Human vitamin D re
20	768	30.8	438	18	W32536 Constitutively act
21	768	30.8	438	20	W93902 Human CAR receptor
22	763	30.6	348	14	R41346 Human CAR receptor
23	733.5	29.4	357	20	Y17872 Mouse nuclear rece
24	725	29.1	358	20	W93903 Mouse CAR receptor
25	676	26.3	356	19	W37251 Rat vitamin D rece
26	656	26.3	356	20	W94622 Rat vitamin D rece
27	632	25.3	367	14	R43656 Human ubiquitinous n
28	500.5	20.1	460	16	R74738 Human ubiquitinous n
29	500.5	20.1	461	15	R52980 Human recombinant
30	500.5	20.1	461	17	R97982 Human steroid rece
31	500.5	20.1	461	17	R98140 NER receptor poten
32	498.5	20.0	445	21	Y32374 Mouse CNRER-1. Mu
33	498	20.0	460	18	W25034 Human ubiquitinous n
34	497.5	19.9	461	17	R62334 Human foetal lung
35	491.5	19.7	447	17	W03326 LXR-alpha, orphan
36	480	19.6	446	17	R99736 OR-1 orphan recept
37	488	19.6	446	17	R94159 Rat ubiquitinous nuc
38	483.5	19.4	443	16	R74739 Rat ubiquitinous nuc
39	483.5	19.4	443	18	W25035 XR2. Homo sapiens
40	481.5	19.3	440	14	R33744 Human retinoid rec
41	472.5	18.9	472	19	W40072 Farnesoid-activate
42	461	18.5	469	17	W03448 Human retinoid rec
43	457.5	18.3	757	20	W71297 EGR polypeptide su
44	455.5	18.3	757	19	W18603 Lucifla cuprina ec
45	452.5	18.1	484	17	R97935 Retinoid X recepto

ALIGNMENTS

RESULT 1	
Y25411	Y25411 standard; Protein; 473 AA.
XX	Y25411;
AC	
XX	
XX	06-SEP-1999 (first entry)
DT	
XX	
DE	Human nmr7-1 protein.
XX	
KW	nmr7; nmr7-1; nuclear trans-acting receptor protein; human; regulator;
KW	identification; downstream target gene; cell proliferation;
KW	cell development.
XX	
OS	Homo sapiens.
XX	
PN	W09931129-AA.
XX	
PD	24-JUN-1999.
XX	
PE	11-DEC-1998; 98MO-US26364.
XX	
PR	14-OCT-1998; 98US-0104251.
PR	12-DEC-1997; 97US-0069401.
XX	
PA	(MERI) MERCK & CO INC.
XX	
PI	Chen F;
XX	
XX	WPI: 1999-405024/34.
DR	N-PSDB; X78808.
XX	
PT	DNA encoding human nuclear receptors nmr7 and nmr7-1
XX	
PS	Claim 20; Fig 6; 80pp; English.

XX This invention describes the isolation of the novel human nuclear
 CC receptors nmr7 or nmr7-1. The nmr7 and nmr7-1 proteins are useful in
 CC the identification of downstream target genes and ligands regulating its
 CC activity. The nuclear receptor is involved in the regulation of in vivo
 CC cell proliferation and/or cell development. The nmr7 and nmr7-1
 CC polynucleotides, expression vectors and host cells are useful for the
 CC recombinant production of the protein.

XX Sequence 473 AA;

Query Match 100.0%; Score 2494; DB 20; Length 473;
 Best Local Similarity 100.0%; Pred. No. 7.3e-237;
 Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVTHTHFKGSLRAPALPLHSAALASNHPRPEANLEVRPKESWNHADVHCEDTE 60
 DB 1 mvtvrtthfkgsrlrapalplhsaaaelasnhprpeanlevrpkesswnhadvhcedte 60
 QY 61 SVPGKPSVNADEEVGPOICRVCGDKATGYHFNWVTCEGCKGFRRAMKRNARLRCFPRK 120
 DB 61 svpgkpsvnadeevgpgqicrvcgdkatgyhfnwvtcegcgkgtfrramkrtnarlrpcfrk 120
 QY 121 GACETTRTRROCCACRLKCLSESGMKKEMIMSDAEVERRALIKRKKSERTGTOPGVQ 180
 DB 121 gacetttrtrrqccacrlkclesgmkkemmimsdaveerrallikrkksertgtqpvq 180
 QY 181 GLTEEQMMIMRELMDAOKTFTDTSFHKNFRLPGVLSGCCPELSQAPSRERAAKWSQ 240
 DB 181 glteeqmmimrelmdaoktftdtsfhknfrlpgvlsngcelpesiqapsreaaakwsq 240
 QY 241 VRKDLCSLKYSLQLRGEGSVWNTKPPADSGKRTFSLPHMADMSTYMKKGIISPAKYI 300
 DB 241 vrkdlsclksylqrgedgsvwnkppadsgkrtfslphmadmstymkkgiistakyl 300
 QY 301 SYFRDLPIEDQISILKGAFAELCOLRENTVFNATGTWECGRLSYCLEDTAGGFQOLLLE 360
 DB 301 syfrdlpliedqisilkgafaelcolrntvfnatgtwecgrlsyccledtaggfqollle 360
 QY 361 PMLKFNHMKKILQHEEYVLMQALISFSPDRPGVLOHRVVDQLOEQFAITLKSIECNR 420
 DB 361 pmkfnhmkkllqheeeylmqalislspdrpgvlohrrvvdqlqeqfaiatlksiecnr 420
 QY 421 POPAHRFLFKIMAMLETLSINAQHTORLRIODIHFPATPLMOELFGITGS 473
 DB 421 ppaahrflfkimamletlsinaqhtqrlriidihfpatplmoelfgitgs 473

RESULT 2

ID Y15936 standard; Protein; 473 AA.

XX Y15936;

04-AUG-1999 (first entry)

DE A human intranuclear receptor protein.

KW Human; intranuclear receptor protein; drug development; diagnosis;
 treatment.

OS Homo sapiens.

XX JP11127872-A.

PD 18-MAY-1999.

PF 07-AUG-1998; 98JP-0224172.

PR 11-AUG-1997; 97JP-0230335.

XX (NIBS) JAPAN TOBACCO INC.

XX MPI: 1999-350330/30.
 DR N-PSDB; X59974.

PT New intranuclear receptor protein - useful for drug development and
 diagnosis and treatment of disease

PS Disclosure; Page 32-35; 38pp; Japanese.

CC The present sequence represents a human intranuclear receptor protein.
 CC The nucleic acid sequence was isolated from a human adult cDNA
 CC library using a swedish ANO23 derived probe. The protein can
 CC be used for the development of drugs and diagnosis and treatment
 CC of various diseases.

XX Sequence 473 AA;

Query Match 100.0%; Score 2494; DB 20; Length 473;
 Best Local Similarity 100.0%; Pred. No. 7.3e-237;
 Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVTHTHFKGSLRAPALPLHSAALASNHPRPEANLEVRPKESWNHADVHCEDTE 60
 DB 1 mvtvrtthfkgsrlrapalplhsaaaelasnhprpeanlevrpkesswnhadvhcedte 60
 QY 61 SVPGKPSVNADEEVGPOICRVCGDKATGYHFNWVTCEGCKGFRRAMKRNARLRCFPRK 120
 DB 61 svpgkpsvnadeevgpgqicrvcgdkatgyhfnwvtcegcgkgtfrramkrtnarlrpcfrk 120
 QY 121 GACETTRTRROCCACRLKCLSESGMKKEMIMSDAEVERRALIKRKKSERTGTOPGVQ 180
 DB 121 gacetttrtrrqccacrlkclesgmkkemmimsdaveerrallikrkksertgtqpvq 180
 QY 181 GLTEEQMMIMRELMDAOKTFTDTSFHKNFRLPGVLSGCCPELSQAPSRERAAKWSQ 240
 DB 181 glteeqmmimrelmdaoktftdtsfhknfrlpgvlsngcelpesiqapsreaaakwsq 240
 QY 241 VRKDLCSLKYSLQLRGEGSVWNTKPPADSGKRTFSLPHMADMSTYMKKGIISPAKYI 300
 DB 241 vrkdlsclksylqrgedgsvwnkppadsgkrtfslphmadmstymkkgiistakyl 300
 QY 301 SYFRDLPIEDQISILKGAFAELCOLRENTVFNATGTWECGRLSYCLEDTAGGFQOLLLE 360
 DB 301 syfrdlpliedqisilkgafaelcolrntvfnatgtwecgrlsyccledtaggfqollle 360
 QY 361 PMLKFNHMKKILQHEEYVLMQALISFSPDRPGVLOHRVVDQLOEQFAITLKSIECNR 420
 DB 361 pmkfnhmkkllqheeeylmqalislspdrpgvlohrrvvdqlqeqfaiatlksiecnr 420
 QY 421 POPAHRFLFKIMAMLETLSINAQHTORLRIODIHFPATPLMOELFGITGS 473
 DB 421 ppaahrflfkimamletlsinaqhtqrlriidihfpatplmoelfgitgs 473

RESULT 3

ID Y15933 standard; Protein; 473 AA.

XX Y15933;

04-AUG-1999 (first entry)

DE A human intranuclear receptor protein.

KW Human; intranuclear receptor protein; drug development; diagnosis;
 treatment.

OS Homo sapiens.

XX JP11127872-A.

PD 18-MAY-1999.

XX 07-AUG-1998; 98JP-0224172.
 XX 11-AUG-1997; 97JP-0230335.
 XX (NISB) JAPAN TOBACCO INC.
 XX WPI; 1999-350330/30.
 XX N-PSDB; X59968.
 DR New intranuclear receptor protein - useful for drug development and
 DR diagnosis and treatment of disease
 PT Claim 2; Page 17-19; 38pp; Japanese.
 PS The present sequence represents a human intranuclear receptor protein.
 CC The nucleic acid sequence was isolated from a human adult cDNA
 CC library using a wellfish ANO23 derived probe. The protein can
 CC be used for the development of drugs and diagnosis and treatment
 CC of various diseases.
 CC
 XX Sequence 473 AA:

Query Match 100.0%; Score 2494; DB 20; Length 473;
 Best Local Similarity 100.0%; Pred. No. 7.3e-237;
 Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTYRTHHREGSLRPAALPLHSAAEELASNHPRGPEANLEVRPKSNVHADFCEDTE 60
 DB 1 mvttrthhregslrpaalpshaaeelaalnprgpeanlevrpkswndfvhcedte 60
 QY 61 SVPGKPSVNADEEVGPGQICRVCGDKATGYNHFWMTCEGCKGFFRRAMRNARLCPFRK 120
 DB 61 svpgkpsvnaadeevgpgqicrvcgdkatgyhnmfwmtcecgckgffrramrnlcpfrk 120
 QY 121 GACETTRKTRRQOCACRLKCLSESGKKEMKMSDAVEERRALIRKKSERTGTOPLQVQ 180
 DB 121 gacetrtrktrrqocacrlkclsesgkkmksdaveerralirkksergtgtoplqvq 180
 QY 121 gacetrtrktrrqocacrlkclsesgkkmksdaveerralirkksergtgtoplqvq 180
 DB 121 gacetrtrktrrqocacrlkclsesgkkmksdaveerralirkksergtgtoplqvq 180
 QY 181 GTEBORMMIRELMDAOMKFTDTFSHPFNRLPGVLSGCELPESLOAPSRBAKXSO 240
 DB 181 gteebormmirelmdaomkftdtfshpfnrlpgvlsgeclpeslqapsrbaakxso 240
 QY 241 VRKDLCSLKVSQLRGDEGSVWNYKPPADSGKEIFSLPHNADSTYFKGIISFAFYI 300
 DB 241 vrkdlsclkvsqlrgegsvwnykppadsgkeifslphnadstyfkgiisfayyi 300
 QY 301 SYFRDLPIDQISLKGAAFEICQLRFNTVNAETGTEGRLSYCLEDTAGGFOQLLLE 360
 DB 301 syfrdlpidqisllkgaafeicqlrfntvnaetgtwecgrlsycltdtaggfgqllle 360
 QY 361 PULKRFYMKKIKQLHBEENVLMQALSTSPDRGVLQHRVYDQLOEOGRIATLKSTIEENR 420
 DB 361 pulkrfymkkikqlhbeenvlmqalstspdrvgvlqhrvydqloegriatlkstieenr 420
 QY 421 POPARHFEFLKIMAMLTSLASINAQHTORLRIQDIHFFAPFLMDELGITGS 473
 DB 421 poparhfeflkimaltelsinaqhtorlriqidihffapflmdegitgs 473
 DB 421 poparhfeflkimaltelsinaqhtorlriqidihffapflmdegitgs 473
 RESULT 4
 ID Y09516 standard; Protein; 473 AA.
 XX Y09516;
 AC 16-JUL-1999 (first entry)
 DT Human vitamin D receptor related gamma 2 protein.
 DE Human vitamin D receptor related protein; VDRR; obesity; diabetes;
 XX Human; vitamin D receptor related protein; VDRR; obesity; diabetes;
 XX anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia;
 KW

KW hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; tumour;
 KW hyperproliferative skin disorder; hyperthyroidism.
 OS Homo sapiens.
 XX KO9919354-A1.
 PN 22-APR-1999.
 PD 31-AUG-1998; 98WO-SR01548.
 PE 31-MAR-1998; 98SE-0001148.
 PR 14-OCT-1997; 97SE-0003745.
 PA (PHAA) PHARMACIA & UPJOHN AB.
 PI Berkenstem A, Dahlberg M;
 XX WPI; 1999-302508/25.
 DR N-PSDB; X56243.
 XX
 PT New vitamin D receptor related (VDRR) polypeptides useful for
 PT treating obesity, diabetes, anorexia and rheumatoid arthritis
 PS Claim 19; Page 22-24; 35pp; English.
 PS The present sequence is a human vitamin D receptor related (VDRR)
 CC polypeptide. Human VDRR polypeptides and substances which affect VDRR
 CC signal transduction, can be used for treating metabolic, proliferative
 CC or inflammatory conditions. They can be used in the manufacture of a
 CC medicament for treating the following conditions: obesity, diabetes,
 CC anorexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or
 CC hyperlipoproteinaemia and osteoporosis, rheumatoid arthritis, benign and
 CC malign tumours, hyperproliferative skin disorders or hyperthyroidism.
 CC Nucleic acid vectors encoding for expression of a VDRR polypeptide can
 CC be used for treating metabolic, proliferative or inflammatory conditions,
 CC by introducing them into a mammal. The introduced nucleic acid is then
 CC capable of transforming a cell in vivo and then polypeptide is expressed.
 CC A substance affecting VDRR signal transduction, such as an agonist or
 CC antagonist can be used for the manufacture of a medicament for treating
 CC metabolic, proliferative or inflammatory condition.
 CC N.B. The specification specifically claims the VDRR nucleic acid and
 CC polypeptide sequences given in figures 1, 4, 7 and 8, but no figures
 CC are given in the specification.
 CC
 XX Sequence 473 AA:

Query Match 100.0%; Score 2494; DB 20; Length 473;
 Best Local Similarity 100.0%; Pred. No. 7.3e-237;
 Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTYRTHHREGSLRPAALPLHSAAEELASNHPRGPEANLEVRPKSNVHADFCEDTE 60
 DB 1 mvttrthhregslrpaalpshaaeelaalnprgpeanlevrpkswndfvhcedte 60
 QY 61 SVPGKPSVNADEEVGPGQICRVCGDKATGYNHFWMTCEGCKGFFRRAMRNARLCPFRK 120
 DB 61 svpgkpsvnaadeevgpgqicrvcgdkatgyhnmfwmtcecgckgffrramrnlcpfrk 120
 QY 121 GACETTRKTRRQOCACRLKCLSESGKKEMKMSDAVEERRALIRKKSERTGTOPLQVQ 180
 DB 121 gacetrtrktrrqocacrlkclsesgkkmksdaveerralirkksergtgtoplqvq 180
 QY 181 GTEBORMMIRELMDAOMKFTDTFSHPFNRLPGVLSGCELPESLOAPSRBAKXSO 240
 DB 181 gteebormmirelmdaomkftdtfshpfnrlpgvlsgeclpeslqapsrbaakxso 240
 QY 241 VRKDLCSLKVSQLRGDEGSVWNYKPPADSGKEIFSLPHNADSTYFKGIISFAFYI 300
 DB 241 vrkdlsclkvsqlrgegsvwnykppadsgkeifslphnadstyfkgiisfayyi 300
 QY 301 SYFRDLPIDQISLKGAAFEICQLRFNTVNAETGTEGRLSYCLEDTAGGFOQLLLE 360

```

DB 301 syfdiediedisllkkaafelqrlntvfnctwecgrlssycladagsgfqlle 360
QY 361 PMLFHYMKRLQHEEEYVLMQAIISLSPDRPGVLOHRVVDQLOEQFAITLKSYIECNR 420
DB 361 pmkfhymllkllqheeeylmqaislspdrpgvlghrvvdqldgeqfaiitksylecnr 420
QY 421 PQPHRFLFKIMAMLTFLRSINAOHTORLRIODIHFPATPLMOELFGITGS 473
DB 421 pqphrflfkimamltelrsinaqhnqrllrlqldhfpatplmgelfgits 473

RESULT 5
ID Y16035
AC Y16035;
DE 04-AUG-1999 (first entry)
XX
XX
XX 04-AUG-1999 (first entry)
DE A human intranuclear receptor protein.
XX
XX Human; intranuclear receptor protein; drug development; diagnosis;
XX treatment.
XX
XX Homo sapiens.
XX
XX JP1127872-A.
XX
XX 18-MAY-1999.
XX
XX 07-AUG-1998; 98JP-0224172.
XX
XX 11-AUG-1997; 97JP-0230335.
XX
XX (NISR ) JAPAN TOBACCO INC.
XX
XX WPI: 1999-350330/30.
XX
XX N-PSDB: X59975.
XX
XX
XX New intranuclear receptor protein - useful for drug development and
XX diagnosis and treatment of disease
XX
XX Disclosure; Page 35-37; 38pp; Japanese.
XX
XX
XX The present sequence represents a human intranuclear receptor protein.
XX The nucleic acid sequence was isolated from a human adult cDNA
XX library using a swillfish ANO23 derived probe. The protein can
XX be used for the development of drugs and diagnosis and treatment
XX of various diseases.
XX
XX
XX Sequence 457 AA;

Query Match 93.6%; Score 2334; DB 20; Length 457;
Best Local Similarity 98.7%; Pred. No. 3.8e-221;
Matches 443; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

```

QY 265 KPPADSGKEIFSLPLPHADMSYFKGIISFAKVISYFRDLPIEDQISLLKGAPELQ 324
DB 249 kppadsgkeifslplphadmsyfkglisfakvisyfrdlpiedqisllkgafelc 308
QY 325 LNFNTVNAETGTCWEGRLSYCLEDETFAGFQOLLLEPMKFHYMKRLQHEEEYVLMQ 384
DB 309 lfnvtnaetgwcgrlssycladagsgfqllepmkfhymllkllqheeeylmq 368
QY 385 ISLSPDRPGVLOHRVVDQLOEQFAITLKSYIECNRPQPHRFLFKIMAMLTFLRSINA 444
DB 369 islspdrpgvlghrvvdqldgeqfaiitksylecnrpqphrflfkimamltelrsina 428

QY 445 OHTORLRIODIHFPATPLMOELFGITGS 473
DB 429 ohtorlrlriodihfpatplmgelfgits 457

RESULT 6
ID Y15932
AC Y15932;
DE 04-AUG-1999 (first entry)
XX
XX
XX 04-AUG-1999 (first entry)
DE A human intranuclear receptor protein.
XX
XX Human; intranuclear receptor protein; drug development; diagnosis;
XX treatment.
XX
XX Homo sapiens.
XX
XX JP1127872-A.
XX
XX 18-MAY-1999.
XX
XX 07-AUG-1998; 98JP-0224172.
XX
XX 11-AUG-1997; 97JP-0230335.
XX
XX (NISR ) JAPAN TOBACCO INC.
XX
XX WPI: 1999-350330/30.
XX
XX N-PSDB: X59967.
XX
XX
XX New intranuclear receptor protein - useful for drug development and
XX diagnosis and treatment of disease
XX
XX Claim 2; Page 16-17; 38pp; Japanese.
XX
XX
XX The present sequence represents a human intranuclear receptor protein.
XX The nucleic acid sequence was isolated from a human adult cDNA
XX library using a swillfish ANO23 derived probe. The protein can
XX be used for the development of drugs and diagnosis and treatment
XX of various diseases.
XX
XX
XX Sequence 457 AA;

Query Match 93.6%; Score 2334; DB 20; Length 457;
Best Local Similarity 98.7%; Pred. No. 3.8e-221;
Matches 443; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

```

Db 129 gmkkemlmsdeaveerrallkrkksertgtplyvgqiteeqmmrlmdagmktfdtt 188
OY 205 FSHKFNRLPGVLSGGCELPESLQAPREBAKMSQVRKDLCSLKYSLOLGRDGSVMNY 264
Db 189 fshfnfrlpgvlsaggcelpeslqapsrebaakmsqvirkdcslkvslqtrgedgsvmny 248
OY 265 KPPADSGGKEITSLPHMADSTYMKGIISFAKVISYRDLPIEDQISLKGAAFEICQ 324
Db 249 kppadsggkeifslipmadmslymkglisfakvisyfrldpliedqslkgaafelcq 308
OY 325 LRFNTVNAETGTCGRLSYCLEDTAGGPOQLLEPMKHYMLKTKQLHEEYVLMQA 384
Db 309 lrfntvnaetgwcgrlsyccledtaggfgqlllepmlkhymlkqlheeyvlmqa 368
OY 385 ISLSPDRPGVLOHRVVDLOEOPAITLKSYTECNRPQPAHRLFLKIMAMTELSINA 444
Db 369 islsfdrpgvlyqhrvvdqlgeqfaeltksylecnrppahrfllkimalteltsina 428
OY 445 OHTQRLRIODIHPRATPLMOELFGITGS 473
Db 429 qhtqrlrldqihpafatplmgelfgltgs 457

RESULT 7
Y25410
ID Y25410 standard; Protein; 466 AA.
XX
AC Y25410;
XX
DT 06-SEP-1999 (first entry)
XX
DE Human nNR7 partial protein.
XX
KW nNR7; nNR7-1; nuclear trans-acting receptor protein; human; regulator;
KW identification; downstream target gene; cell proliferation;
KW cell development.
XX
OS Homo sapiens.
XX
PN MO9931129-A1.
XX
PD 24-JUN-1999.
XX
PF 11-DEC-1998; 98WO-US26364.
XX
PR 14-OCT-1998; 98US-0104251.
XX
PR 12-DEC-1997; 97US-0069401.
XX
PA (MERI) MERCK & CO INC.
XX
PI Chen F;
XX
DR WPI: 1999-405024/34.
DR N-PSDB; X78807.
XX
PT DNA encoding human nuclear receptors nNR7 and nNR7-1
XX
PS Claim 1; Fig 3; 80pp; English.
XX
CC This invention describes the isolation of the novel human nuclear
CC receptors nNR7 or nNR7-1. The nNR7 and nNR7-1 proteins are useful in
CC the identification of downstream target genes and ligands regulating its
CC activity. The nuclear receptor is involved in the regulation of in vivo
CC cell proliferation and/or cell development. The nNR7 and nNR7-1
CC polynucleotides, expression vectors and host cells are useful for the
CC recombinant production of the protein.
XX
SO Sequence 466 AA;

```

Query Match 93.6%; Score 2334; DB 20; Length 466;
 Best Local Similarity 98.7%; Pred. NO. 3.9e-221;

```

Matches 443; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
OY 25 AELIASNHPGPDEANTLEVPRKSNHADFVHCETTESVPGKPSVNDDEVGQIQIRVCG 84
Db 18 aknlppspgipseanleripkesvnhdfvhcedtesvpkpsvnddevgpqlcrvsg 77
OY 85 DKATGYHHNVMTGSCGCGFFPRANKRNARLRCPPRGACETIRKTRROCCARLRKLES 144
Db 78 dkatgyhhnvmtcgscgckgffprankrnaarlrcpprgacetiirktrrqccarlrkles 137
OY 145 GMKKEIMSEAVEERRALTRKKSERTGQPIGVGCTFEQKMMRLMDAOMKTFDIT 204
Db 138 gmkkemlmsdeaveerrallkrkksertgtplyvgqiteeqmmrlmdagmktfdtt 197
OY 205 FSHKFNRLPGVLSGGCELPESLQAPREBAKMSQVRKDLCSLKYSLOLGRDGSVMNY 264
Db 198 fshfnfrlpgvlsaggcelpeslqapsrebaakmsqvirkdcslkvslqtrgedgsvmny 257
OY 265 KPPADSGGKEITSLPHMADSTYMKGIISFAKVISYRDLPIEDQISLKGAAFEICQ 324
Db 258 kppadsggkeifslipmadmslymkglisfakvisyfrldpliedqslkgaafelcq 317
OY 325 LRFNTVNAETGTCGRLSYCLEDTAGGPOQLLEPMKHYMLKTKQLHEEYVLMQA 384
Db 318 lrfntvnaetgwcgrlsyccledtaggfgqlllepmlkhymlkqlheeyvlmqa 377
OY 385 ISLSPDRPGVLOHRVVDLOEOPAITLKSYTECNRPQPAHRLFLKIMAMTELSINA 444
Db 378 islsfdrpgvlyqhrvvdqlgeqfaeltksylecnrppahrfllkimalteltsina 437
OY 445 OHTQRLRIODIHPRATPLMOELFGITGS 473
Db 438 qhtqrlrldqihpafatplmgelfgltgs 466

RESULT 8
Y15931
ID Y15931 standard; Protein; 434 AA.
XX
AC Y15931;
XX
DT 04-AUG-1999 (first entry)
XX
DE A human intranuclear receptor protein.
XX
KW Human; intranuclear receptor protein; drug development; diagnosis;
KW treatment.
XX
OS Homo sapiens.
XX
PN JP1127872-A.
XX
PD 18-MAY-1999.
XX
PF 07-AUG-1998; 98JP-0224172.
XX
PR 11-AUG-1997; 97JP-0230335.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
DR WPI: 1999-350330/30.
DR N-PSDB; X59966.
XX
PT New intranuclear receptor protein - useful for drug development and
PT diagnosis and treatment of disease
XX
PS Claim 1; Page 15-16; 38pp; Japanese.
XX
CC The present sequence represents a human intranuclear receptor protein.
CC The nucleic acid sequence was isolated from a human adult cDNA
CC library using a swallfish ANO23 derived probe. The protein can
CC be used for the development of drugs and diagnosis and treatment
CC of various diseases.

```


XX Sequence 434 AA:

Query Match 91.8%; Score 2289; DB 20; Length 434;
Best Local Similarity 100.0%; Pred. No. 9,5e-217;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

40 LEVPRKESWNADVFYHEDPESVGRKPSVNADEEVGSPQICRGCKATGHHNVTCEG 99
1 LEVPRKESWNADVFYHEDPESVGRKPSVNADEEVGSPQICRGCKATGHHNVTCEG 60
100 CKGFRRAMKNNARLRCFPRGACETIRKTRRQCOACRLKCLSGMKKMMINSDEAVEE 159
61 CKGFRRAMKNNARLRCFPRGACETIRKTRRQCOACRLKCLSGMKKMMINSDEAVEE 120
160 RRALIKRKKSERTGTPQPGVGLTEQPMRLREMDAOMTFDTTFSEHFNRLPGVLS 219
121 RRALIKRKKSERTGTPQPGVGLTEQPMRLREMDAOMTFDTTFSEHFNRLPGVLS 180
220 GCELPESIQAPSRERAAKMSQVRKDLCSLKVSLQLRGDSGVWNYKPPADSGGKEIFSL 279
181 GCELPESIQAPSRERAAKMSQVRKDLCSLKVSLQLRGDSGVWNYKPPADSGGKEIFSL 240
280 PHMADSTYMPKGIISFAKVISYFRDLPIEDQISLTKGAFAELCOLRNTVFNAETGWE 339
241 PHMADSTYMPKGIISFAKVISYFRDLPIEDQISLTKGAFAELCOLRNTVFNAETGWE 300
340 CGRLSTCLDEDZAGGFQOILLPEMLKFHYMLKQLHEEYVLMQALISFSPDRPGVLOHR 399
301 CGRLSTCLDEDZAGGFQOILLPEMLKFHYMLKQLHEEYVLMQALISFSPDRPGVLOHR 360
400 VVDQLOEOPAITLKSYIECNRPQAPARFLFKIMAMTELINSINAOHTQRLRIQDIHPF 459
361 VVDQLOEOPAITLKSYIECNRPQAPARFLFKIMAMTELINSINAOHTQRLRIQDIHPF 420
460 ATPLMOELFGITGS 473
421 ATPLMOELFGITGS 434

RESULT 9
Y09515
ID Y09515 standard; Protein: 437 AA.
XX
AC Y09515;
XX
DT 16-JUL-1999 (first entry)
DE Human vitamin D receptor related gamma protein.
XX
KW Human; vitamin D receptor related protein; VDRR; obesity; diabetes;
anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia;
hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; tumour;
hyperproliferative skin disorder; hyperthyroidism.
XX
OS Homo sapiens.
XX
PN W09919354-A1.
XX
PD 22-APR-1999.
XX
PF 31-AUG-1998; 98MO-SF01548.
XX
PR 31-MAR-1998; 98SE-0001148.
PR 14-OCT-1997; 97SE-0003745.
XX
PA (PAAA) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Dahlberg M;
XX
DR WPI: 1999-302508/25.
DR N-PSDB; X56242.

XX New vitamin D receptor related (VDRR) polypeptides, useful for
PT treating obesity, diabetes, anorexia and rheumatoid arthritis
PS
XX Claim 19; Page 19-20; 35pp; English.

CC The present sequence is a human vitamin D receptor related (VDRR)
CC polypeptide. Human VDRR polypeptides and substances which affect VDRR
CC signal transduction, can be used for treating metabolic, proliferative
CC or inflammatory conditions. They can be used in the manufacture of a
CC medicament for treating the following conditions: obesity, diabetes,
CC anorexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or
CC hyperlipoproteinaemia and osteoporosis, rheumatoid arthritis, benign and
CC malignant tumours, hyperproliferative skin disorders or hyperthyroidism.
CC Nucleic acid vectors encoding for expression of a VDRR polypeptide can
CC be used for treating metabolic, proliferative or inflammatory conditions,
CC by introducing them into a mammal. The introduced nucleic acid is then
CC capable of transforming a cell in vivo and then polypeptide is expressed.
CC A substance affecting VDRR signal transduction, such as an agonist or
CC antagonist can be used for the manufacture of a medicament for treating
CC metabolic, proliferative or inflammatory condition.
CC N.B. The specification specifically claims the VDRR nucleic acid and
CC polypeptide sequences given in figures 1, 4, 7 and 8, but no figures
CC are given in the specification.

Sequence 437 AA:

Query Match 91.7%; Score 2287; DB 20; Length 437;
Best Local Similarity 99.8%; Pred. No. 1,5e-216;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

40 LEVPRKESWNADVFYHEDPESVGRKPSVNADEEVGSPQICRGCKATGHHNVTCEG 99
1 LEVPRKESWNADVFYHEDPESVGRKPSVNADEEVGSPQICRGCKATGHHNVTCEG 60
100 CKGFRRAMKNNARLRCFPRGACETIRKTRRQCOACRLKCLSGMKKMMINSDEAVEE 159
61 CKGFRRAMKNNARLRCFPRGACETIRKTRRQCOACRLKCLSGMKKMMINSDEAVEE 120
160 RRALIKRKKSERTGTPQPGVGLTEQPMRLREMDAOMTFDTTFSEHFNRLPGVLS 219
121 RRALIKRKKSERTGTPQPGVGLTEQPMRLREMDAOMTFDTTFSEHFNRLPGVLS 180
220 GCELPESIQAPSRERAAKMSQVRKDLCSLKVSLQLRGDSGVWNYKPPADSGGKEIFSL 279
181 GCELPESIQAPSRERAAKMSQVRKDLCSLKVSLQLRGDSGVWNYKPPADSGGKEIFSL 240
280 PHMADSTYMPKGIISFAKVISYFRDLPIEDQISLTKGAFAELCOLRNTVFNAETGWE 339
241 PHMADSTYMPKGIISFAKVISYFRDLPIEDQISLTKGAFAELCOLRNTVFNAETGWE 300
340 CGRLSTCLDEDZAGGFQOILLPEMLKFHYMLKQLHEEYVLMQALISFSPDRPGVLOHR 399
301 CGRLSTCLDEDZAGGFQOILLPEMLKFHYMLKQLHEEYVLMQALISFSPDRPGVLOHR 360
400 VVDQLOEOPAITLKSYIECNRPQAPARFLFKIMAMTELINSINAOHTQRLRIQDIHPF 459
361 VVDQLOEOPAITLKSYIECNRPQAPARFLFKIMAMTELINSINAOHTQRLRIQDIHPF 420
460 ATPLMOELFGITGS 473
421 ATPLMOELFGITGS 434

RESULT 10
Y21799
ID Y21799 standard; Protein: 434 AA.
XX
AC Y21799;
XX
DT 14-SEP-1999 (first entry)
XX

DE Human steroid and xenobiotic receptor (SXR).
 XX
 KW Nuclear receptor; SXR; steroid and xenobiotic receptor; RXR; human;
 KW retinoid X receptor; P450 gene; steroid hormone; steroid metabolism;
 KW phycoerythrin; calcium-channel blocker; steroid toxicity; tuberculosis;
 KW breast cancer; osteoporosis; Cushing syndrome; vitiligo; hirsutism;
 KW polycystic ovarian disease; cancer; colorectal; prostatic.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 227 /Label= unknown
 FT /note= "encoded by ACN"
 XX
 PN W09935246-A1.
 XX
 PD 15-JUL-1999.
 XX
 PF 08-JAN-1999; 99WO-US00490.
 XX
 PR 09-JAN-1998; 98US-0005286.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Blumberg B, Evans RM;
 XX
 DR MPI: 1999-419349/35.
 DR N-PSDB: X89080.
 XX
 PT New steroid and xenobiotic receptor, used to identify modulators for
 PT controlling metabolism of steroids and xenobiotics, e.g. reducing
 PT their toxicity
 XX
 PS Claim 4; Fig 1A; 83pp; English.
 XX
 CC The invention relates to a novel nuclear receptor polypeptide, designated
 CC SXR (steroid and xenobiotic receptor). SXR (1) forms a heterodimer with
 CC retinoid X receptor (RXR), (11) binds to a direct or inverted repeat
 CC response element motif based on the half-site AGTCA, (11) activates
 CC transcription through response elements present in steroid-inducible P450
 CC genes, in response to a wide variety of natural and synthetic steroid
 CC hormones and (1V) is prominently expressed in liver and intestine. SXR
 CC regulates expression of catabolic enzymes, in response to many different
 CC steroids, and thus affects metabolism. SXR is a broad specificity, low-
 CC affinity receptor for reducing excessive levels of steroids in the
 CC circulation. (Ant)agonists of SXR are used to regulate metabolism of
 CC steroids particularly phytoestrogens or calcium-channel blockers, to
 CC reduce steroid toxicity in subjects being treated with steroids, e.g. in
 CC cases of tuberculosis (treated with rifampin and related compounds),
 CC breast cancer (treated with tamoxifen, raloxifen etc.), or osteoporosis
 CC (treated with Vitamin K), or to slow metabolism of therapeutic steroids.
 CC Also, modulating endogenous SXR is used to treat disease, particularly
 CC an agonist is used where endogenous steroid levels are excessive (e.g.
 CC Cushing syndrome; vitiligo and hirsutism in women; polycystic ovarian
 CC disease; 11 beta-, 17- or 21-hydroxylase deficiency; 3 beta-hydroxysteroid
 CC dehydrogenase deficiency, or breast, colorectal or prostatic cancer).
 CC While antagonists are used where endogenous steroid levels are too low.
 CC Cells that express SXR are used to identify compounds likely to be
 CC involved in undesirable drug interactions. Antibodies specific for SXR
 CC are used in immunohistochemical testing for studying distribution/
 CC expression density of SXR, also for diagnosis and therapeutically as
 CC antagonist. The present sequence represents SXR polypeptide.
 XX
 SO Sequence 434 AA:

Query Match 87.0%; Score 2171; DB 20; Length 434;

Best Local Similarity 95.9%; Pred. No. 3.8e-205;

Matches 416; Conservative 2; Mismatches 16; Indels 0; Gaps 0;

QY 40 LEVRKESNADVFHCEPTSEVPRKPSVNDDEYGVGQICVCCDKATGHPNMTGEG 99
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 levrkeswrvhadfvhcedesvypkpsvnaadeevgpgqlcrvcdkalyhfnvmtceg 60
 QY 100 CKGFFRRAMRNARLCPFRKACETTRKTRROCCARLKLKESGKKRKMIMSDAYPE 159
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 ckgffrramrnarlcpfrkacetrtrktrroccarlklkessgkkmimdsdaavee 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 160 RRLAIRKKSEKRTGTPPLGVQGLTEQRMKIRELMDAQKTDYTFSHKRNRLPGVLSS 219
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 rrlairkkseertgtplgvqglteeqrmkirelmdaqtftfshknfrlpgvlss 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 220 GCELPESLOAPSRBAKMSQVKKDCSLKVSQRLGDEGQSWNNYPPADSGKEIFSL 279
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 gcelpeplqpsrbaakmsqvrkdcslkvsqrgldeqswnnypadsgkeifsl 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 280 PHMADNKTVEFKGISFAKYSYFRDLPEDQISLKGAEFELCOLFRFTVNAETGTE 339
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 phmadnktvfkglisfakysyfrdplpqdqlslkgaeefelcolfrftvnaetgve 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 340 CGRLSTCLEETAGGFQOLLEPMLKFRHYMLKQLHSEEVYLMQALSLSPDRPGVLAQR 399
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 cgrlstcleetaggfqqlllepmlkfrhymlkqlhseevylmqalslspdrpgvlgqr 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 400 VVDQLOEQFAITKSYTECVRPOPANRFLFKIMAMLTSLRSINAGTQRLRLRIDIHFF 459
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 vvdqlqeqfaeltksytecvrpopanrflfkimamltslrsinaeqhtrllridihpf 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 460 ATPLMQELFCITGS 473
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 atplmqelfcigtgs 434

RESULT 11

ID Y42691 standard; Protein: 414 AA.

AC Y42691;

DT 17-JAN-2000 (first entry)

DE Human pregnane X receptor (hPXR).

KW Human; nuclear receptor; pregnane X receptor; PXR; CYP; CYP3A4;

KX cytochrome P-450 mono-oxygenase; drug interaction; hPXR.

OS Homo sapiens.

PN W09948915-A1.

PD 30-SEP-1999.

PF 26-MAR-1999; 99WO-US06737.

PR 27-MAR-1998; 98US-0079593.

PA (GLAX) GLAXO GROUP LTD.

PI Kilewer SA, Willson TM;

DR MPI: 1999-601202/51.

DR N-PSDB: Z07997.

PT New human pregnane X receptor, used to identify specific modulators and

agents that induce expression of cytochrome P-450 mono-oxygenase

PS Claim 4; Fig 1A-D; 69pp; English.

CC The invention provides an isolated human nuclear receptor (designated
 CC pregnane X receptor, PXR) that binds to a cytochrome P-450 mono-oxygenase
 CC (CYP) promoter. The hPXR is used to identify its specific modulators,
 CC and compounds that induce CYP3A4 expression (i.e. to identify drug
 CC interactions, since CYP3A4 is involved in many biotransformations of
 CC drugs). The modulators are potentially useful for: associating particular
 CC diseases and conditions with PXR and for treating such conditions.

CC Antibodies raised against hpxr can be used for determination and
CC purification of hpxr. The present sequence represents the hpxr.

XX Sequence 414 AA;

Query Match 86.9%; Score 2167; DB 20; Length 414;
Best Local Similarity 95.4%; Pred. No. 8.8e-205;
Matches 414; Conservative 0; Mismatches 0; Indels 20; Gaps 1;

QY 40 LEVRKESWNRADYVHCEDTESVPGKSVNADDEVGQICRVCGRATGTHNVMTCEG 99
DB 1 LEVRKESWNRADYVHCEDTESVPGKSVNADDEVGQICRVCGRATGTHNVMTCEG 60
QY 100 CKGFPRMRNRARLRGCFRRKACETIRKTRROCOACLRRCLESGMKKEMINSDAEVVE 159
DB 61 CKGFPRMRNRARLRGCFRRKACETIRKTRROCOACLRRCLESGMKKEMINSDAEVVE 120
QY 160 RRAIIKKRKSERTGTOPPLGVGLTEQGRMIRLMDAQMTFTTFSHFKNRFLPGVLS 219
DB 121 RRAIIKKRKSERTGTOPPLGVGLTEQGRMIRLMDAQMTFTTFSHFKNRFLPGVLS 180
QY 220 GCELPESIQADSRREAAKWSQVRKDLCSLKVSLQLRGDSVWNYKRPADSGKEIRSL 279
DB 181 GCELPESIQADSRREAAKWSQVRKDLCSLKVSLQLRGDSVWNYKRPADSGKEIRSL 240
QY 280 PHMDMSYVNFKGIISFPAKVSYPFDLPIDEOISLKGAEFLCOLFNTVFNATGTE 339
DB 241 PHMDMSYVNFKGIISFPAKVSYPFDLPIDEOISLKGAEFLCOLFNTVFNATGTE 300
QY 340 CGRLSYCLEDTAGFQOULLPMLKFHYMLKKQLHBEVYLMQAISLSPDRPGVLOHR 399
DB 301 CGRLSYCLEDTAGFQOULLPMLKFHYMLKKQLHBEVYLMQAISLSPDRPGVLOHR 360
QY 400 VVDLOQEOFAITLKYTCNRPQAPARFLFKIMAMTELRSINAQTRQLRIQDIHPF 459
DB 361 VVDLOQEOFAITLKYTCNRPQAPARFLFKIMAMTELRSINAQTRQLRIQDIHPF 400
QY 460 ATPLMQELFGITGS 473
DB 401 ATPLMQELFGITGS 414

RESULT 12

Y42689
ID Y42689 standard; Protein; 316 AA.

XX Y42689;

DT 17-JAN-2000 (first entry)

DE His6-pregnane X receptor (PXR) sequence.

KW Human; nuclear receptor; pregnane X receptor; PXR; CYP; CYP3A4;
KW cytochrome P-450 mono-oxygenase; drug interaction; hpxr.

OS Synthetic.

OS Homo sapiens.

PN W09948915-A1.

PD 30-SEP-1999.

PE 26-MAR-1999; 99WO-US06737.

PR 27-MAR-1998; 98US-0079593.

PA (GLAXO) GLAXO GROUP LTD.

PI Kilewer SA, Willson TM;

DR WPI; 1999-601202/51.

PI New human pregnane X receptor, used to identify specific modulators and
PI agents that induce expression of cytochrome P-450 mono-oxygenase
XX
XX Example 6; Page 37; 69pp; English.

CC The invention provides an isolated human nuclear receptor (designated
CC pregnane X receptor, PXR) that binds to a cytochrome P-450 mono-oxygenase
CC (CYP) promoter. The hpxr is used to identify its specific modulators,
CC and compounds that induce CYP3A4 expression (i.e. to identify drug
CC interactions, since CYP3A4 is involved in many biotransformations of
CC drugs). The modulators are potentially useful for associating particular
CC diseases and conditions with PXR and for treating such conditions.
CC Antibodies raised against hpxr can be used for determining and
CC purification of hpxr. The present sequence represents a histidine-6
CC tagged partial PXR (His6-PXR) sequence.

XX Sequence 316 AA;

Query Match 63.6%; Score 1585; DB 20; Length 316;
Best Local Similarity 100.0%; Pred. No. 1e-147;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 SERTGTOPPLGVGLTEQGRMIRLMDAQMTFTTFSHFKNRFLPGVLSGCELPESIQ 228
DB 12 SERTGTOPPLGVGLTEQGRMIRLMDAQMTFTTFSHFKNRFLPGVLSGCELPESIQ 71
QY 229 APSREAAKWSQVRKDLCSLKVSLQLRGDSVWNYKRPADSGKEIRSLPHMDMSY 288
DB 72 APSREAAKWSQVRKDLCSLKVSLQLRGDSVWNYKRPADSGKEIRSLPHMDMSY 131
QY 289 MFKGIISFPAKVSYPFDLPIDEOISLKGAEFLCOLFNTVFNATGTE 348
DB 132 MFKGIISFPAKVSYPFDLPIDEOISLKGAEFLCOLFNTVFNATGTE 191
QY 349 DTAGSFQOULLPMLKFHYMLKKQLHBEVYLMQAISLSPDRPGVLOHRVVDLOQEO 408
DB 192 DTAGSFQOULLPMLKFHYMLKKQLHBEVYLMQAISLSPDRPGVLOHRVVDLOQEO 251
QY 409 AITLKYTCNRPQAPARFLFKIMAMTELRSINAQTRQLRIQDIHPATPLMQLF 468
DB 252 AITLKYTCNRPQAPARFLFKIMAMTELRSINAQTRQLRIQDIHPATPLMQLF 311
QY 469 GITGS 473
DB 312 GITGS 316

RESULT 13

R98521
ID R98521 standard; Protein; 386 AA.

AC R98521;

DT 14-NOV-1996 (first entry)

DE Xenopus orphan receptor 6.

KW Xenopus orphan receptor 6; XOR-6; steroid receptor; vitamin D;
KW hydroxybenzoate; mercaptobenzoate; aminobenzoate.

XX Xenopus laevis.

OS

FH Key Location/Qualifiers

FT Domain /Label= DNA_binding_domain

FT Domain /Label= 183..386

PN W09622390-A1.

PD 25-JUL-1996.

PF 16-JAN-1996; 96WO-US00058.
 XX
 PR 17-JAN-1995; 95US-0374445.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Blumberg B, Evans RM, Umeson K;
 XX
 DR WPI; 1996-354546/35.
 DR N-PSDB; T36499.
 XX
 PT DNA encoding receptor polypeptide responsive to hydroxy, mercapto or
 PT amino benzoate(s) - useful to regulate gene transcription
 PS
 PS Claim 4; Page 27-28; 42pp; English.
 CC
 CC Xenopus orphan receptor 6 (XOR-6) (R98521) is a new member of the
 CC steroid receptor superfamily, characterized as being responsive to
 CC the presence of hydroxy, mercapto or amino benzoate(s) and as
 CC regulating the transcription of associated gene(s). It shows 73%
 CC identity in the DNA binding domain, and 42% identity in the ligand
 CC binding domain, to the human vitamin D receptor. Recombinant XOR-6
 CC can be expressed in animal cells; a cDNA clone (T36499) coding for
 CC XOR-6 has been isolated. The recombinant XOR-6 may be used to
 CC regulate gene transcription or to raise antibodies of diagnostic
 CC or therapeutic appln.
 CC
 XX
 XX Sequence 386 AA;
 SQ

Query Match 39.3%; Score 979.5; DB 17; Length 386;
 Best Local Similarity 48.6%; Pred. No. 5.1e-88;
 Matches 202; Conservative 60; Mismatches 105; Indels 49; Gaps 9;

QY 57 EDTSVPGKPSVADNEVGPQICRVGDKATGYHFNVTCEGKGFRRAMKRNALNC 116
 DB 14 eeedaanscgtdedgdgpkicracgdratgyhfnantcegcgffrravrnrlisc 73
 QY 117 PFRKACETIRKTRROCOACRLKCLSGMKKEMSDAVERALLIRK-RSERTGTQ 175
 DB 74 pf-qnsclvlnknrricqecrclkkclidgmrkclmsdaavegrallkrkhkltklp 132
 QY 176 PLGVGGLTEORVMRELMDAOKTDTFSHFNKRLPGLVLSGCELPESLQAPRENA 235
 DB 133 pppa-altpedqbficqlvgahcktdfifskntr-----plr--- 171
 QY 236 AKWSQVRKDLCSLKSLSQLRGDEGSVWNYKPPADSGKKEIFSLPHAMDMSTYMKGIS 295
 DB 172 -----rsadpt---qepqets---seafimlphladlvymkqlls 207
 QY 296 FAVISYFRDLPREDQISLKGAFELCOLRFTVFNAGETGWEGRSLSYCLEDT-AGGF 354
 DB 208 fammlyfifslidedqiallkgsvaeavylrftvfnadlnwecgpfydeedmlagf 267
 QY 355 QOQLLEPMKLFHMLKRLQLEHEEYVLMQALISFSPDRPGVLQHRVYDLOEQAFITLKS 414
 DB 268 rqlflepjvrlhmmmklnvgaeeyammaalafasyrpyvcdwekqlqghlaltlkd 327
 QY 415 YIECNR-PPAHREFLFKTAMLTETRSINAQHTORLRIODIHFPARPLMQLRG 469
 DB 328 fidsqppspqrnllypkimeclteitrvndhskqlllelwdlqdpdrlmzevg 383

RESULT 14
 W94623
 ID W94623 standard; Protein; 423 AA.
 XX
 AC W94623;
 XX
 DT 29-APR-1999 (first entry)
 XX
 DE Rat vitamin D receptor protein VDR0.
 XX

KM Vitamin D receptor; VDR: bone density; retinoic acid derivative;
 KM steroid; bone calcium regulator; immunosuppressant; anticancer.
 XX
 OS Rattus sp.
 XX
 PN W09856908-AL.
 XX
 PD 17-DEC-1998.
 XX
 PF 13-JUN-1997; 97WO-JP02052.
 XX
 PR 13-JUN-1997; 97WO-JP02052.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Kato S, Ueno K;
 XX
 DR WPI; 1999-080898/07.
 DR N-PSDB; X16606.
 XX
 PT Gene for vitamin D receptor isoform protein which blocks vitamin D
 PT signal pathway - and production of recombinant isoform protein using
 PT it, for bone density assay and for screening compounds for vitamin D
 PT activity.
 PS
 PS Example 1; Fig 1; 47pp; Japanese.
 XX
 CC The present invention describes rat vitamin D receptor (VDR) isoform
 CC protein VDR1. The present sequence represents rat VDR0. VDR1 differs
 CC from the canonical form of VDR (VDR0) by lacking the amino acid sequence
 CC encoded by exon 9, but instead substitutes a short sequence
 CC (GTEPGEEELRDIGHVQDE in the rat protein) encoded by the 5'-end of Intron
 CC 8. VDR1 has a dominant negative effect on the vitamin D signalling
 CC pathway. The isoform protein can be used for determining bone density,
 CC and for the screening of compounds (e.g. steroids and retinoic acid
 CC derivatives) for vitamin D activity (e.g. as bone calcium regulators,
 CC immunosuppressants or anticancer agents).
 CC
 XX
 XX Sequence 423 AA;
 SQ

Query Match 32.1%; Score 801; DB 20; Length 423;
 Best Local Similarity 42.0%; Pred. No. 2.1e-70;
 Matches 172; Conservative 75; Mismatches 135; Indels 28; Gaps 9;

QY 77 POICRVGDKATGYHFNVTCEGKGFRRAMKRNALRCRPFKACETIRKTRROCOAC 136
 DB 21 plicvgcgdratgyhfnantcegcgffrramkrlfcpf-ngdrcrlkdnrrhcgac 79
 QY 137 RLKRLSGMKKEMSDAVERALLIRKRSERTGTQPLGVGGLTEORVMRELMDA 196
 DB 80 rlcrcvdlgmkkellldeevqkrtemlnrkeeeakdsrlrp-lseegqnlallda 138
 QY 197 QMKTFTTFSFKNFRPLPGVL--SSGCELPESLQAPRENAKWSQVRKDLCSLV--- 250
 DB 139 hbktydptyadfditfrpvmtdsgtsyspr---plsfsgnssasdsalysltsldme 194
 QY 251 -----SLQLRGDEGSVWNYKPPADSGKKEIFSLPHAMDMSTYMKGISYFRD 305
 DB 195 psgfnsdlidngedd-----dpsvclldlplsmhphladlvyslqkvlgfakmlygfid 249
 QY 306 LPREDQISLKGAFELCOLRFTVFNAGETGWEGRSLSYCLEDT--AGGFQOQLLEPM 362
 DB 250 ltsddqivllksaalevmlrnsqsfmdmsdvcgsqdykyvdtvskaghlellep 309
 QY 363 LKRFHMLKRLQLEHEEYVLMQALISFSPDRPGVLQHRVYDLOEQAFITLKSIECNRPQ 422
 DB 310 lkrtvgllkxlnlneevylmalclvspdpipyvcdaklvealqdrlnslqlytcrhbp 369
 QY 423 PAHREFLFKTAMLTETRSINAQHTO--RLRRIQDHPF-APPLMQLRG 469
 DB 370 pshbqlyakmlqladlrslneehakysrlsfqpsnsmklpvlvavg 419

```

RESULT 15
W47509
ID W47509 standard; Protein; 423 AA.
XX
AC W47509;
XX
DE 26-JUN-1998 (first entry)
XX
DE Rat vitamin D receptor (VDR).
XX
XX Rat; vitamin D receptor; isoform protein; VDR1; VDR0; diagnosis;
XX dominant negative receptor; signal transmission channel;
XX bone density disorder; screening.
XX
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT Misc-difference 360 /note="encoded by CAC"
FT
XX
XX MO9747172-A1.
XX
PD 18-DEC-1997.
XX
XX 10-JUN-1997; 97WO-IB00947.
XX
XX 10-JUN-1996; 96JP-0194179.
XX
XX (CHUS ) CHUGAI PHARM CO LTD.
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Kato S, Ueno K;
XX
XX WPI; 1998-051917/05.
XX N-PSDB; V03129.
XX
XX DNA encoding a vitamin D receptor isoform protein - useful for bone
XX density determination and for screening substances for vitamin D
XX activity
XX
XX PS Disclosure; Fig 1; 46pp; Japanese.
XX
XX A novel cDNA sequence encodes the rat vitamin D receptor isoform
XX protein (VDR1). The isoform differs from the normal receptor
XX (VDR0), which comprises the present sequence, in having the
XX vitamin D response element curtailed by 86 residues, and having an
XX extra 19 residues inserted at the C-terminal of this element. It
XX acts as a dominant negative receptor in the vitamin D signal
XX transmission channel.
XX The isoform protein can be used to diagnose bone density disorders,
XX and screen for substances having potential vitamin D-like activity.
XX
XX Sequence 423 AA;

```

```

Query Match 32.0%; Score 798; DB 19; Length 423;
Best Local Similarity 42.0%; Pred. No. 4,2e-70;
Matches 172; Conservative 74; Mismatches 136; Indels 28; Gaps 9;

```

```

OY 77 PQCRCVCGDKATGCHYFNVTCEGCKGFFRRAMRNALRCPFRKACETTRTRRQCAC 136
DB 21 prlgvgcdrtatgfinamtecgckgffirmkraltcpf-ngdcritkdnrrhcqac 79
OY 137 RLKRCLESGMKEMIMSDAVERRALIKKKSEKRTGTPGLVGGTPEQRMTRELMDA 196
DB 80 rlkrcvcdigmmefflldeevqkrkemlmkrkeeealldslrpx-lseeqhilaillda 138
OY 197 QMKTEDTFESHKRNRLGVV--SSGCELPESLQAPSRREAKMSQVRKDCSLKV--- 250
DB 139 hnktydpcyadrtidrrpymdsgyspr-----plsfsgnsssssdlytcladme 194
OY 251 -----SLQLRGDEGSVMWYKPPADSGGKEIFSLPLPHMADMTYMKGIISFAKYISYFRD 305

```

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DB 195 psgfsmldngedsd-----dpvltldlspismplhpadlvsyldgkygafakmipgrfd 249
OY 306 LPREDQISLKGAAFEICQURFNTVENAETGTECGRLSYCLEDT---AGGFOQLLEPM 362
DB 250 ltsddqivllkssalevilmrnsqsfmdmswcdsgsdydydvltavskaghtlelepl 309
OY 363 LKPHYMLKTLQHEEYVLMQATSLFSPDRPGYLQHRVVDLOEQPAILTKSYIECNRPQ 422
DB 310 ikrgvylkknllneehvllmalcivspdrpgvdaklvealqdrlnslgtylrcrthpp 369
OY 423 PAHRFLFKTAMLTLEKRSINAQHTQ--RLLRIGDIHPF-ATPLMQDLRG 469
DB 370 psgbqlyakmqladlrslneehskyzslsfqpensmkltpdlvlevly 419

```

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Search completed: February 18, 2001, 14:29:40
Job time: 8217 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2001, 14:35:36 ; Search time 3075.67 Seconds

(without alignments)
6618.640 Million cell updates/sec

Title: US-09-143-828-1

Perfect score: 2905
Sequence: 1 cctctgaaggctctagaatc.....aaaaaaaaaaaaaaaaaaaaa 2905

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: gb_est8:*
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 174: em_estp73:*
 175: em_estp74:*
 176: em_estp75:*
 177: em_estp76:*
 178: em_estp77:*
 179: em_estp78:*
 180: em_estp79:*
 181: em_estp80:*
 182: em_estp81:*
 183: em_estp82:*
 184: em_estp83:*
 185: em_estp84:*
 186: em_estp85:*
 187: em_estp86:*
 188: em_estp87:*
 189: em_estp88:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523.2	18.0	638	38	AV651714
2	445.2	15.3	461	10	AA699679
3	416	14.3	454	13	N94132
4	370.8	12.8	794	24	A1746915
5	343	11.8	343	18	A1248626
6	335	11.5	365	143	N69311
7	201	6.9	472	4	AA277370
8	199.6	6.9	493	96	AM871811
9	185.4	6.4	200	10	AA679591
10	166.4	5.7	463	91	AM511148
11	165.4	5.7	215	31	AV108557
12	156.8	5.4	432	40	AM158294
13	154.4	5.3	601	40	AM107536
14	143.8	5.0	560	24	A1768052
15	140.8	4.8	1053	110	BE573656
16	132.8	4.6	540	38	AM012320
17	132	4.5	463	15	AI049299
18	118	4.1	724	15	AI046425
19	108.4	3.7	468	6	AA396982
20	102	3.5	463	2	AA107961
21	101.2	3.5	506	10	AA679391
22	100.8	3.5	616	17	A1238397
23	99.2	3.4	732	28	AJ393915
24	99	3.4	370	15	AI024672
25	99	3.4	507	4	AA264990
26	97.6	3.4	690	106	BE266478
27	97.6	3.4	1105	107	BE410116
28	97.2	3.3	589	106	BE275249
29	94	3.2	851	137	BE877201
30	90.2	3.1	708	107	BE390042
31	88.8	3.1	692	135	BE791424
32	88.6	3.0	392	91	AM505439
33	88.6	3.0	475	111	BE664197
34	86.6	3.0	539	16	AI098643
35	83.6	2.9	623	106	BE303050
36	83.4	2.9	788	137	BE915476
37	82.8	2.9	665	107	BE390515
38	82.4	2.8	467	9	AA570839
39	81.8	2.8	959	137	BE903117
40	81.4	2.8	564	37	AV609965
41	81.2	2.8	771	107	BE385638
42	81	2.8	248	4	AA272757
43	81	2.8	514	2	AA124058
44	80.4	2.8	667	87	AM231123
45	80	2.8	563	105	BE233303

ALIGNMENTS

RESULT 1
 AV651714
 LOCUS AV651714 638 bp mRNA
 DEFINITION AV651714 GIC Homo sapiens cDNA clone GICCS03 3', mRNA sequence.
 ACCESSION AV651714
 VERSION AV651714.1 GI:9872728
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens.

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.jnl.gov) for further information.
MGI:994718

Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 472.

FEATURES

source

1..794
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone_1b="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
/note="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTC); Site 2: DraIII (CACCATGTC); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [GTGTGGCTTCTG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTC, 3' site CACCATGTC). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
BASE COUNT 206 a 180 c 253 g 152 t 3 others
ORIGIN

Query Match 12.8%; Score 370.8; DB 24; Length 794;
Best Local Similarity 79.3%; Pred. No. 1.4e-75;

Matches 451; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 179 ctgtatcgatccttgcacggatgtgtcaagtggaccccgaggagtcgagacaa 238
DB 229 CTGGCGAGAACCATCTCTCTCAAGTGTGAGACCCCAAGGGGAAATCCAA 288
QY 239 agactaccacacacagcagtcgaagggcccgaaagcacttgagtgagacccaa 298
DB 289 AGCAGTGGCCCCAGACACTGTAGACACACAGATTAACCTTAAGATGACACTGAG 348
QY 299 aaagctggaacacatgtctgtacactgtgagagacacagagtcgtctctgaaagc 358
DB 349 AGAGCTGGAGCGAGTGGCTTGTACACTGTGAAGAACACACCTGCTTGGAGAGC 408
QY 359 ccagtgcaacgagatgagagagtcggaggtcccaaatctgcgtgtatgtgggaca 418
DB 409 CCA--TCAACGTAGAGGAGGAAGATGAGGTCTTCAATCTGCGTGTATGTGGGACA 465
QY 419 agggccacgtggtacacacatgtatgacatgtgaagagatgaaaggtctttcaga 478
DB 466 AGGCAATGGCTACCACTTCAATGTATAGCTGTGAAGAGCAAGGGGTTTTCAGAA 525
QY 479 gggcactgaaacgcaacgcccggctgaggtgccccttcggaaaggcgccctgagatca 538
DB 526 GGGCCATGAAGCATGTCCGGCTGAGGTGCCCTTCGCAAGGAACTCGAGATCA 585
QY 539 cccggaaagccggcgagatgcagagcctgcgcctcgcgcaagtgtcctggaagcgga 598
DB 586 CCCGGAGACAGACGACGCTCCAGGCTCCGCTTCCGCAAGTCCCGAGAGATGACA 645
QY 599 tgaagagagagatgatactgacgagagcggtggaagagggggggtcttgatcaga 658
DB 646 TGAAGAAAGATGATCATGATCCGATCCGCTGTGAGAGAGGGGGCTTGTATCAAGA 705
QY 659 ggaagaaagatgaaacgagagacacagcactgagagtgcaagggcgatgaaagagac 718
DB 706 GGAAGAAAGAGGGAANAGATTGAGGCTCCACGCGCTGGAGAGGAGANNGCTGACGAGAAAC 765
QY 719 agcgatgatgatcaggaagctgataggac 747

DB 766 AGCAAGCGCTGATCCAGAGCTGATGAC 794

RESULT 5
AI248626/c
LOCUS
DEFINITION
AI248626 343 bp mRNA EST 01-DEC-1998
gb77b12.x1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA
clone IMAGE:185067 3' similar to gb:003258 VITAMIN D3 RECEPTOR
(HUMAN); mRNA sequence.

ACCESSION
AI248626
VERSION
AI248626.1 GI:3844023
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 343)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
CONTACT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.jnl.gov) for further information.
Insert Length: 608 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 338.
Location/Qualifiers

FEATURES

source

1..343
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:185067"
/clone_1b="Soares fetal liver spleen INFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (empicillin resistant)"
/note="Organ: Liver and Spleen; Vector: p773D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; This is a subcloned version of the original Soares fetal liver spleen INFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGAGATTAATTAAGATCTTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 56 a 108 c 93 g 86 t
ORIGIN

Query Match 11.8%; Score 343; DB 18; Length 343;
Best Local Similarity 100.0%; Pred. No. 3.4e-69;

Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 cagtcgaagggcccgagaaacacctgagagtgagacccaagaagcctggaacatgc 314
DB 343 CAGTCCAAAGGGCCCAAGAACCAACCTGGAGTGAGACCCCAAGAAAGCTGGAACATGC 284
QY 315 tgacttgatcactgtgagagacacagagtgctctcgaaagccagtgtaaacgaga 374
DB 283 TGACTTGTACACTGTGAGAGACAGAGTGTCTCTGGAAACCCCAAGTCAACCA 224
QY 375 tgaagagtgagaggttcccaaaatctgcgtgtatgtgggaaagggccactgcatca 434
DB 223 TGAAGAGTGGAGGTGCCCAAAATCTGCCGTGTATGTGGGAGCAAGGCCACTGCTATCA 164
QY 435 cttaaatgcatgacatgtgaagatgcaagggcctttcagaagggccatgaacgaa 494
DB 163 CTTCATATGTCATGACATGTGAAGATGCAAGGCGCTTTTTCAGAGAGGCCATGAACGCAA 104

QY 495 cccccgtgtagtggtgcccccttcggaagggcgctgagatcacccggaagaccggggc 554
 Db 103 CGCCGGGTGAGGTGCCCCCTTCGCCGAAGGGCGCTCGAGATCACCCGGAAGACCCGGCG 44
 QY 555 acagtgcagagccctgcgcgcctgcgaagtgcttgagagcgcc 597
 Db 43 ACACTGCCAGGCCCTGCCGCTCGGCGCAAGTGCCTGAGAGAGCGGC 1

RESULT 6
 LOCUS N69311 365 bp mRNA EST 13-MAR-1996
 DEFINITION ra2506.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
 IMAGE:293626 3', mRNA sequence.
 ACCESSION N69311
 VERSION N69311.1 GI:1225472
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 365)
 AUTHORS Haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 TITLE The Washu-Mercx EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: ml3 -40 forward
 High quality sequence stop: 279.

FEATURES
 SOURCE Location/Qualifiers
 1..365
 /organism="Homo sapiens"
 /db_xref="GDB:3801473"
 /db_xref="taxon:9606"
 /clone="IMAGE:293626"
 /clone_lib="Soares fetal liver spleen INFLS"
 /sex="Male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: Liver and Spleen; Vector: pRT73D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGCAAGATTAATTAAGATCTTTTCTTTTCTTTTCTTTT 3'] double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pRT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaudo."

BASE COUNT 95 a 106 c 68 g 95 t 1 others
 ORIGIN

Query Match 11.5%; Score 335; DB 143; Length 365;
 Best Local Similarity 97.0%; Pred. No. 2.5e-67;
 Matches 352; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
 QY 2354 aaggagaaatgatataatgacaaaagc-agcacaaggaattccctgtgtgtagtctgag 2412
 Db 365 AAAGGAGAAATGATTAAGTACAAAGCAACCAAGAAATTTCCCTGTGTGATGCTGAG 306
 QY 2413 ctgtgtagtgcagcagctgtgtgtaccgaagtgagttcccgagacatgagctcttagag 2472
 Db 305 CTGTGATGCGCGGCACTGCGGTACCAAGTGAAGGTTCCCGAGGACATGATGCTGTAGAG 246

QY 2473 caaggacacaactgcagctgtgagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2532
 Db 245 CAAGGAGCAAACTGCACACTGTGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGT 186
 QY 2533 gccactgtatggggcctgt 2552
 Db 185 GGCACGTGATGAGGCGCTGGGCTTGTCTGTGGGGCTGGAATCTGGGTATGCTGTGTGACG 126
 QY 2593 aggtcagctgtgcaatcgtttaaacacccggaagagacatttaacgtaccttat 2652
 Db 125 AAGGTACGCTTACAAATCAAGTTAAACACCGAGAGAACCATTTACTGCACTTATAT 66
 QY 2653 tctgtgtacatctattctcaagctaaaggtatgaagtgctgtgtgtgtgtgtgtgt 2712
 Db 65 TCTGTGTACATCTATCTTCACAAAGCTAAAGCGTATGAAGTGCCTGCTGTATTAG 6
 QY 2713 cca 2715
 Db 5 CCA 3

RESULT 7
 LOCUS AA277370 472 bp mRNA EST 01-APR-1997
 DEFINITION va81a12.f1 Soares mouse NMU Mus musculus cDNA clone IMAGE:73758 5' similar to TR:G410518 G410518 ORPHAN NUCLEAR RECEPTOR OF STEROID/THYROID SUPERFAMILY. ; mRNA sequence.
 ACCESSION AA277370
 VERSION AA277370.1 GI:1917850
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 472)
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Getzel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
 TITLE The Washu-HMT Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 Washu-HMT Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:454806
 Putative full length read
 vector to vector length is 506
 Seq primer: -28ml3 rev2 Et from Amersham.

FEATURES
 source Location/Qualifiers
 1..472
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:737758"
 /clone_lib="Soares mouse NMU"
 /tissue_type="Liver"
 /lab_host="DH10B"
 /note="Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTGAGTGGAGCGCGCGCAATCTTTTCTTTTCTTTTCTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library constructed and normalized by Bento Soares and M. Fatima Bonaudo."

QY 2473 caaggacacaactgcagctgtgagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2532
 Db 245 CAAGGAGCAAACTGCACACTGTGAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGT 186
 QY 2533 gccactgtatggggcctgt 2552
 Db 185 GGCACGTGATGAGGCGCTGGGCTTGTCTGTGGGGCTGGAATCTGGGTATGCTGTGTGACG 126
 QY 2593 aggtcagctgtgcaatcgtttaaacacccggaagagacatttaacgtaccttat 2652
 Db 125 AAGGTACGCTTACAAATCAAGTTAAACACCGAGAGAACCATTTACTGCACTTATAT 66
 QY 2653 tctgtgtacatctattctcaagctaaaggtatgaagtgctgtgtgtgtgtgtgtgt 2712
 Db 65 TCTGTGTACATCTATCTTCACAAAGCTAAAGCGTATGAAGTGCCTGCTGTATTAG 6
 QY 2713 cca 2715
 Db 5 CCA 3

Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomimaga, N.,
Matanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M.,
Morimatsu, M., Okazaki, Y. and Hayashizaki, Y.
Riken Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-research-riken.go.jp

Thermofabilitation and thermostabilization of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (<http://genome.riken.go.jp>) for
further details.

FEATURES

source
1..215
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2510047D01"
/clone_1lb="Mus musculus liver C57BL/6J 13-day embryo"
/sex="mixed"
/tissue_type="liver"
/dev_stage="13-day embryo"
BASE COUNT 48 a 60 c 69 g 38 t
ORIGIN

Query Match 5.7%; Score 165.4; DB 31; Length 215;
Best Local Similarity 85.6%; Pred. No. 5.5e-26;
Matches 184; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 443 tcatgacatggaagatgcaagagcttttcagagagccatgaagcagcccgccg 502
DB 1 tcttgacccctgacagatgacagagcccttttcagagagcccttgacacacatgctccg 60
QY 503 tgaagtgcccttcggaagagcgctgagatcacccggaagacccggaagagtcg 562
DB 61 tgaagtgcccttcggaagagcgctgagatcacccggaagacccggaagagtcg 120
QY 563 agagctgagcctgagcagatgctgagagcgagcagatgaagagagatgcatgctgcg 622
DB 121 agcctgagcctgagcagatgctgagagcgagcagatgaagagagatgcatgctgcg 180
QY 623 acgagcgctggaagagagcgagcctgagcagag 657
DB 181 atgcccctgtgagcagcagcagcagcctgagcagag 215

RESULT 12

AM158294 432 bp mRNA EST 05-NOV-1999
LOCUS AM158294
DEFINITION za39e07.x1 Xenopus EST library Xenopus laevis cDNA clone za39e07
ACCESSION AM158294
VERSION AM158294.1 GI:6270323
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis

REFERENCE
AUTHORS
TITLE
JOURNAL
Expressed sequence tags from Xenopus
Unpublished (1999)

COMMENT

Contact: W. Richard McCombie
Lita Anenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: rcombie@cshl.org
Plate: za39 row: e column: 07
Seq primer: M13 universal forward primer
High quality sequence stop: 432.

FEATURES

source
1..432
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="za39e07"
/clone_1lb="Xenopus EST library"
/tissue_type="total brain tissue"
/cell_line="W22-RGA"
/dev_stage="tadpole"
/note="Vector: lambda Zap I; Site 1: XbaI. This library
was supplied by Holly Cline (Cold Spring Harbor Labs).
cDNA synthesis with oligo dt Xba I (Xba I cloning site).
RNA: stage 50-56 tadpoles, total brain tissue, CTC
extraction method."
BASE COUNT 112 a 90 c 142 g 88 t
ORIGIN

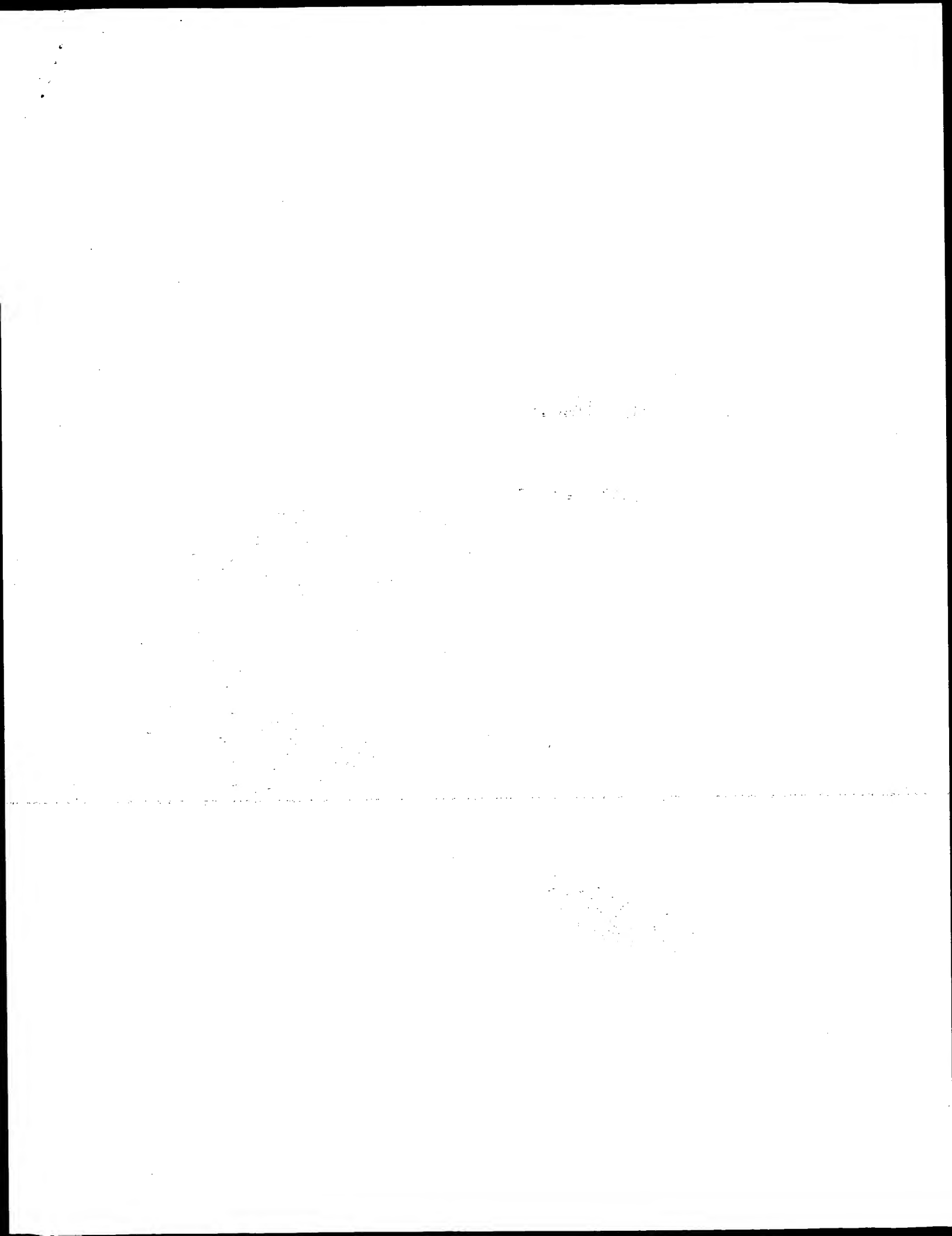
Query Match 5.4%; Score 156.8; DB 40; Length 432;
Best Local Similarity 74.0%; Pred. No. 6.4e-26;
Matches 213; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 370 ggaatggaagatgcaagagccttcacaaatcgcgtatgtagggagcagccactgac 429
DB 147 gaaagcag 206
QY 430 taccatcattatgcatgacatgagagagagagagagagagagagagagagagagag 489
DB 207 ttttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 266
QY 490 gcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 549
DB 267 agcaatctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 323
QY 550 cggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 609
DB 324 cggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 383
QY 610 atgacatgctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 657
DB 384 ttgacatgctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 431

RESULT 13

AM107536 601 bp mRNA EST 20-OCT-1999
LOCUS AM107536
DEFINITION u91a06.y1 Sugano mouse kidney mK1a Mus musculus cDNA clone
IMAGE:2159410.5 similar to gb:J03258 VITAMIN D3 RECEPTOR (HUMAN);
gb:U15548 Mus musculus beta 2 thyroid hormone receptor (MOUSE);
mRNA sequence.
ACCESSION AM107536
VERSION AM107536.1 GI:6078336
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS
TITLE
JOURNAL
Expressed sequence tags from Xenopus
Unpublished (1999)



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2001, 14:29:41 ; Search time 124.29 Seconds
(without alignments)
3766.761 Million cell updates/sec

Title: US-09-143-828-1

Perfect score: 2905
Sequence: 1 cctctgaaggttcctagatc.....aaaaaaaaaaaaaaaaaaaaa 2905

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_NA.*
2: /cgn2_6/ptodata/2/1na/5A.COMB.seq.*
3: /cgn2_6/ptodata/2/1na/5B.COMB.seq.*
4: /cgn2_6/ptodata/2/1na/6.COMB.seq.*
5: /cgn2_6/ptodata/2/1na/PCrus.COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	278.8	9.6	2043	1	US-07-737-736B-6
2	272.8	9.4	1399	1	US-07-737-736B-5
3	170.6	5.9	1450	1	US-08-458-489-1
4	170.6	5.9	1450	1	US-07-843-350C-1
5	170.6	5.9	1450	1	US-08-646-686-1
6	170.6	5.9	1450	1	US-08-646-686-1
7	97.6	3.4	1898	1	US-08-342-411A-1
8	97.6	3.4	1979	2	US-08-648-619B-1
9	97.6	3.4	2030	1	US-08-330-518-1
10	97.6	3.4	2030	1	US-08-330-283-1
11	97.6	3.4	2030	2	US-08-646-248-1
12	97.6	3.4	2030	4	US-08-646-248-1
13	97.6	3.4	2030	4	US-08-646-248-1
14	97.2	3.3	1813	4	US-08-646-248-1
15	91.4	3.1	2928	2	US-08-646-248-1
16	91.4	3.1	2928	2	US-08-646-248-1
17	91.4	3.1	2928	2	US-08-646-248-1
18	91.4	3.1	2928	2	US-08-646-248-1
19	91.4	3.1	2928	2	US-08-646-248-1
20	91.4	3.1	2928	2	US-08-646-248-1
21	91.4	3.1	2928	2	US-08-646-248-1
22	89.8	3.1	704	2	US-08-592-383-5
23	89.8	3.1	704	2	US-08-592-383-5
24	85.2	2.9	1959	4	US-08-342-411A-3
25	85.2	2.9	1959	4	US-08-342-411A-3
26	83.8	2.9	2558	2	US-08-592-383-3
27	80.8	2.8	1860	4	US-08-372-652-7
28	80.8	2.8	1860	4	US-08-372-652-7

29	79.6	2.7	1659	1	US-08-333-358-7	Sequence 7, Appl
30	79.6	2.7	1659	1	US-08-463-694-7	Sequence 7, Appl
31	79.6	2.7	1659	1	US-08-694-501-7	Sequence 7, Appl
32	77.6	2.7	2970	4	US-08-649-619B-2	Sequence 2, Appl
33	77.6	2.7	1688	2	US-08-466-120-1	Sequence 1, Appl
34	74.8	2.6	1649	2	US-08-466-120-1	Sequence 1, Appl
35	74.8	2.6	1649	2	US-08-466-120-1	Sequence 1, Appl
36	74.4	2.6	1576	5	US-09-144-759-17	Sequence 19, Appl
37	74.4	2.6	2241	3	US-09-144-759-17	Sequence 19, Appl
38	74.4	2.6	2295	3	US-09-144-759-17	Sequence 21, Appl
39	74.4	2.6	2301	3	US-09-144-759-21	Sequence 11, Appl
40	73.2	2.5	2468	1	US-08-333-358-11	Sequence 11, Appl
41	73.2	2.5	2468	1	US-08-463-694-11	Sequence 11, Appl
42	73.2	2.5	2468	1	US-08-694-501-11	Sequence 11, Appl
43	72.6	2.5	1893	5	US-08-694-501-11	Sequence 11, Appl
44	68.6	2.4	1677	2	US-08-372-652-14	Sequence 14, Appl
45	68.6	2.4	1677	2	US-08-372-652-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-07-737-736B-6
Sequence 6, Application US/0773736B
Patent No. 5260199
GENERAL INFORMATION:
APPLICANT: Deluca, Hector F.
APPLICANT: Ross, Troy K.
APPLICANT: Prahl, Jean M.
TITLE OF INVENTION: Method Of Producing
TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESS: Carl R. Schwartz, Esq., c/o Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07737,736B
FILING DATE: 19910730
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Carl R.
REGISTRATION NUMBER: 29,437
TELEPHONE: 414-277-5715
TELEFAX: 414-277-5715
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2043 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rat
PUBLICATION INFORMATION:
AUTHORS: Burmester, James K.
AUTHORS: Wiese, Russell J.
AUTHORS: Maeda, No. 5260199uyuo
AUTHORS: Deluca, Hector F.
TITLE: Structure and regulation of the rat

TITLE: 1,25-dihydroxyvitamin D3 receptor
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 85
PAGES: 9499-9502
DATE: December-1988
US-07-737-736B-6

Query Match 9.6%; Score 278.8; DB 1; Length 2043;
Best Local Similarity 55.6%; Pred. No. 2.9e-53;
Matches 629; Conservative 0; Mismatches 482; Indels 21; Gaps 4;

QY 331 ccccaaatcgcggtgtagtggtgggacaagccactggtatccatccaatgtaatacaca 450
DB 155 ccccgagatctgtagtggtgagacgacgacgacgacgacgacgacgacgacgacgac 214
QY 451 tgtgagagatcgaaggggtttttcagagggccatgaaagcagcccggtcgaagtgcc 510
DB 215 tgtgagagatcgaaggggtttttcagagggccatgaaagcagcccggtcgaagtgcc 274
QY 511 cccctcgcgaagggcgctgcgagagacccgcgaagccgcgagtgccagctgcgctgc 570
DB 275 cccctcgcgaagggcgctgcgagagacccgcgaagccgcgagtgccagctgcgctgc 331
QY 571 cgcctgcgaagtgctgcgagagagagagagagagagagagagagagagagagagag 630
DB 332 cggctcgaagtgctgcgagagagagagagagagagagagagagagagagagagag 391
QY 631 gtgag 690
DB 392 gtgag 451
QY 691 ctgag 750
DB 452 ctgag 508
QY 751 cagatgaag 805
DB 509 cagatgaag 568
QY 806 -ggatgctgaag 864
DB 569 atgag 628
QY 865 gctgcaagtgag 924
DB 629 tcttctcgaag 688
QY 925 cggag 984
DB 689 tccaag 748
QY 985 atcttctcgaag 1044
DB 749 cctctcgaag 808
QY 1045 agcttgcgaag 1104
DB 809 ggccttgcgaag 868
QY 1105 ctgaag 1164
DB 869 ctgaag 928
QY 1165 actgag 1215
DB 929 gattgag 988
QY 1216 ggtgag 1275
DB 989 gctgag 1048
QY 1276 ctgag 1335

DB 1049 CTGAACCTACATGAG 1108
QY 1336 cgcgcag 1395
DB 1109 CGACCTGGGGGCTCCAG 1168
QY 1396 ctgaagctcgaag 1455
DB 1169 CTGACAG 1228
QY 1456 ataatgag 1507
DB 1229 ATGATCCAG 1280

RESULT 2
US-07-737-736B-5
Sequence 5, Application US/073736B
Patent No. 5260199
GENERAL INFORMATION:
APPLICANT: Deluca, Hector F.
APPLICANT: Ross, Troy K.
TITLE OF INVENTION: Method Of Producing
TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carl R. Schwartz, Esq., c/o Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,736B
FILING DATE: 19910730
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Carl R.
REGISTRATION NUMBER: 29,437
REFERENCE/DOCKET NUMBER: 96-296-2185-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 414-277-5715
TELEFAX: 414-277-5774
INFORMATION FOR SPO ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1399 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Baker, Andrew R.
AUTHORS: McDonnell, Donald P.
AUTHORS: Hughes, Mark
AUTHORS: Grisp, Tracey M.
AUTHORS: Mangelsdorf, David J.
AUTHORS: Haussler, Mark R.
AUTHORS: Pike, J. W.
AUTHORS: Shine, John
AUTHORS: O'Malley, Bert W.
TITLE: Cloning and expression of full-length cDNA
TITLE: encoding human vitamin D receptor

JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 85
PAGES: 3294-3298
DATE: May-1988
US-07-737-736B-5

Query Match	9.48;	Score 272.8;	DB 1;	Length 1399;
Best Local Similarity	55.18;	Pred. No. 5.4e-52;		
Matches 638;	Conservative 0;	Mismatches 487;	Indels 33;	Gaps 4

QY	391	cccccaatctgcggtgtatgtgtggtgaaacaaggccacatgctcatcatcttcaatgtgcatgaca	450
Db	176	ccccgatatgttgaggatgtgtgtgaaaccgaccactctgctttccattcattgtgtaaggacc	235
QY	451	tgltgaagatgtcaaaaggccttttccagagaggccaatgaacgcgaagcccgctgaggtgc	510
Db	236	tengaaagctcgaaaggctttcttcagagggaagcattgaagggaagagacatttacccttc	295
QY	511	cccttcgcgaagggcgctctcgagatcaaccggaaagaccggcgagtcagtgccagtcgc	570
Db	296	cccttc---AACGGGGATGGCCGATCAACAAAGACAAACGAGCCACTGCCAGGCGCTGC	352
QY	571	cgccctgcgaatgtgcctgtgagagcgccaatgaagaagatgtatcaatgtctgcagcgcc	630
Db	353	cggcctcaaaacgctgtgtggaatcgccattgattgaaggagttcattctgaaagatgagga	412
QY	631	gt'gagagagagcgcgcccttgatcaagcgagaaagatgaacggaacagaggtaccgca	690
Db	413	gtgcagagagaaagcgggaagatgattcctgaaggcgaaagagagggcgcttgaaaggaact	472
QY	691	ctggagagcgaggggtctgacaaagaaagcagcggtgtgtgtcdgagagcttgatgagcgt	750
Db	473	ctgcg---GCCAMGCTGTCTGAAGACAGAGAGCGCATCTTGCCATTGCTGCTGAGCGCC	529
QY	751	caagatgaaaaccttctgacacacacctctccattccaagaattccggctgcgaaggggtg	810
Db	530	caccattaaagacctgaagaccaccactactccgactctgcgcacagttccggctccagttcgt	589
QY	811	cttagcagtggtcgcgagtgtgcagagtcctctgagggccc-----a	852
Db	590	gtgaattgattgtgagaggagaccatcttccagggcccaactccaagacatccacagcttc	649
QY	853	tcgagggagaaagctctgcgaagtgtgagccaggtccggaagatctgtgcctttgaaggtc	912
Db	650	tctggggaactcctctcctctcctgctcagatcattgattacactcttcaagacattgaggaac	709
QY	913	tctctgcagctgcggggggagaaatgacgtgtcttgaaactacaaaccccaagcgcgaagt	972
Db	710	tctgtcacacttctccattctggaatctgagtgaaagaaagattcagaatcacccttctggaac	769
QY	973	ggcgggaaagagatcctctccctctgcgtgcccaatgctgcgacatgtcacaactacatgttc	1033
Db	770	ctaaagctgtccacgactctccatgctccccaccctgcacacttgcgttaccgaaatc	829
QY	1033	aaaggcatcatcagctcttgcgaaagatcatcttaccctcagaggtcgcacatcgaggac	1092
Db	830	caaaaagctcatttgcttctgcaagatgattacagaaattcagaaacctcactcttagaagac	889
QY	1093	cagatctccctgcgtgaaggggggcgcgcttctcagagctgtcacaactgaaatcaacaagtg	1152
Db	890	cagatctcgaactgctgaaggtcagatgaccattgagaggtatcattgttggtgcctcaatgagctc	949
QY	1153	ttcaagcgagagacttgacatcgagagtggtgtgcggc-----tgtccacagcttg	1203
Db	950	tttcaacatggaagacacatgtctctggaactctgagcgaacaaagacttcaaaagtacggctcagt	1009
QY	1204	gaagacactgcagtggtcttcacgaacattctacatgagagcccatgctgaaattccactac	1263
Db	1010	gacctgacaaagccggagacacagccttgagactgattgagaccctcattcaagttcagaagtg	1069
QY	1264	atgctgaaagagcgctgcagctgcatgtggaggtatgctgtcatgacgacatctccctc	1323

Db 1070 GGACTGAAGAGGCTGAACTTGATGTAGAGAGAGACATGTCCTCTCATGGCCATCTGCATC 11299

QY 1334 tttcccccaacccagccaggtgtgtgtgcagcaacccgctggtyggacacagctygaagagca 13633

Db 1130 GTCTCCCAACATGCTCTGGGGGACAGAGACGCCGCGCTATTGAGGCCATCCAGGACCGC 11899

QY 1384 ttgcacattctctgaagttctacatgtatgtgaatcggtcccccagccctgcacataagtttc 14433

Db 1190 CTGTGCACACACTGCAGAGAGTACATCCGCTGCGGCACCCGCCCGGCGACCACTG 12499

QY 1444 ttgttctcgaagatcctatggtctatgctcaccagatccagatcctcagatcaatgtctcagacc 15033

Db 1250 CTCCTATGCCAGATGATGATCCAGAGCTAGACCCGACCTGCGGAGCGCTCAATGAGAGAGACTCC 13099

QY 1504 cagcgagctgtctgagcatt 1521

Db 1310 AAGCAGTACCGCTGCTC 1327

RESULT 3
US-08-459-489-1
: Sequence 1, Application US/08459489
: Patent NO. 5568574.

```

? GENERAL INFORMATION:
? APPLICANT: David D. Moore et al.
? TITLE OF INVENTION: CAR RECEPTORS AND RELATED
? TITLE OF INVENTION: MOLECULES AND METHODS
? NUMBER OF SEQUENCES: 10
?

```

ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
REF: 00110 2001

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 555X
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: MicriPerfect (Version 5.0)
;
; ORDERING INFORMATION:

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/843,350
FILING DATE: February 26, 1992
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 30,152
REFERENCE/DOCKET NUMBER: 00786/126001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906

```

: INFORMATION FOR SEQ ID NO: 1:
:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 1450.
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear

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US-08-459-489-1

Query Match	5.9%	Score 170.6;	DB 1;	Length 1450;
Best Local Similarity	57.5%;	Pred. NO.3.3e-29;		
Matches 327; Conservative	0;	Mismatches 239;	Indels 3;	Gaps 1

[illegible]

[illegible]

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RESULT 9
US-08-330-518-1
Sequence 1, Application US/08330518
Patent No. 5607967
GENERAL INFORMATION:
APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
APPLICANT: Schmidt, Azriel
APPLICANT: Vogel, Robert.
TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,518
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dolan, Catherine A.
REGISTRATION NUMBER: 36,502
REFERENCE/DOCKET NUMBER: 19316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4283
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ. ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-330-518-1

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Query Match      3.48; Score 97.6; DB 1; Length 2030;
Best Local Similarity 54.8%; Pred. No. 7.1e-13;
Matches 215; Conservative 0; Mismatches 174; Indels 3; Gaps 1.

Oy 314 ctgacttgtaacgtgagacacagagttcttctctggaagcccaagtgtcaacgcag 373

```


TELEPHONE: (908) 594-4283
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-646-248-1

Query Match 3.4%; Score 97.6; DB 2; Length 2030;
Best Local Similarity 54.8%; Pred. No. 7.1e-13;
Matches 215; Conservative 0; Mismatches 174; Indels 3; Gaps 1;

QY 314 ctgacttgtaacactgtgaggaacagagtcgttccctgaaagccagtgtaacgag 373
DB 417 CAGACTGGGTATCCAGATCCGAAAGAGAACAGAGCCGAAAGAGAGGCCAG 476
QY 374 atgaggaagtcgagagtcgcaaatcgcgtgtatgtgaggaagccagtcgtatc 433
DB 477 CCCCAGAGATGCTGGGCCAGACGCTTGGCTGTCTGTGGGACAAAGGCTCCGCTTCC 536
QY 434 acttcaatgtacatgtatgaaagtcgaaagtccttttcaagagggccatgaagcga 493
DB 537 ACTACAAAGTCTCAGCTGCGAAGGCTGCAAGGCTTCTCCGCGCAAGTGTGCTCCG 596
QY 494 agcccgagtcgagtgcccttcggaagggg---cttgagatcacccggaagacc 550
DB 597 GTGGGGCCAGGCTTATGCTGCGGGGAGTGGCGAACTGCGCAAGTGAAGCTTTCATGC 656
QY 551 ggcgaagtcgcaagtcgctgcgcctgcgaagtccttgaaagccgcatgaagaagaga 610
DB 657 GCGGCAAGTCTGCGGCAAGTCTGCGGCAAGTCAAGAGGAGGAGGAGGAGGAGT 716
QY 611 tgatcatgtccgaagagccgtgtgaaagagggccttgatcaagcggaagaaagt 670
DB 717 GCGTCTTTCTGAAGAACAGATCCGGAAGAAAGATTGGAAACAGCAGCAGAGAT 776
QY 671 aacggaagagagtcagccacttgagagtcag 702
DB 777 CACAGTCACAGTCCGACATCACTGTGGGCCG 808

RESULT 12
PCT-US95-13924-1
Sequence 1, Application PC/TUS9513924
GENERAL INFORMATION:
APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
APPLICANT: Rutledge, Su Jane
APPLICANT: Schmidt, Azriel
TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13924

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Quagliato, Carol S.
REGISTRATION NUMBER: 35,330
REFERENCE/DOCKET NUMBER: 19327 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3809
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-13924-1

Query Match 3.4%; Score 97.6; DB 4; Length 2030;
Best Local Similarity 54.8%; Pred. No. 7.1e-13;
Matches 215; Conservative 0; Mismatches 174; Indels 3; Gaps 1;

QY 314 ctgacttgtaacactgtgaggaacagagtcgttccctgaaagccagtgtaacgag 373
DB 417 CAGACTGGGTATCCAGATCCGAAAGAGAACAGAGCCGAAAGAGAGGCCAG 476
QY 374 atgaggaagtcgagagtcgcaaatcgcgtgtatgtgaggaagccagtcgtatc 433
DB 477 CCCCAGAGATGCTGGGCCAGACGCTTGGCTGTCTGTGGGACAAAGGCTCCGCTTCC 536
QY 434 acttcaatgtacatgtatgaaagtcgaaagtccttttcaagagggccatgaagcga 493
DB 537 ACTACAAAGTCTCAGCTGCGAAGGCTGCAAGGCTTCTCCGCGCAAGTGTGCTCCG 596
QY 494 agcccgagtcgagtgcccttcggaagggg---cttgagatcacccggaagacc 550
DB 597 GTGGGGCCAGGCTTATGCTGCGGGGAGTGGCGAACTGCGCAAGTGAAGCTTTCATGC 656
QY 551 ggcgaagtcgcaagtcgctgcgcctgcgaagtccttgaaagccgcatgaagaagaga 610
DB 657 GCGGCAAGTCTGCGGCAAGTCTGCGGCAAGTCAAGAGGAGGAGGAGGAGGAGT 716
QY 611 tgatcatgtccgaagagccgtgtgaaagagggccttgatcaagcggaagaaagt 670
DB 717 GCGTCTTTCTGAAGAACAGATCCGGAAGAAAGATTGGAAACAGCAGCAGAGAT 776
QY 671 aacggaagagagtcagccacttgagagtcag 702
DB 777 CACAGTCACAGTCCGACATCACTGTGGGCCG 808

RESULT 13
PCT-US95-13931-1
Sequence 1, Application PC/TUS9513931
GENERAL INFORMATION:
APPLICANT: Friedman, Eitan
APPLICANT: Holloway, M. Katharine
APPLICANT: Rodan, Gideon
APPLICANT: Rutledge, Su Jane
APPLICANT: Schmidt, Azriel
TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13931
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Quagliato, Carol S.
REGISTRATION NUMBER: 35,330
REFERENCE/DOCKET NUMBER: 19316 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2030 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOHETICAL: NO
ANTI-SENSE: NO
PCT-US95-13931-1

Query Match 3.4%; Score 97.6; DB 4; Length 2030;
Best Local Similarity 54.8%; Pred. No. 7.1e-13;

Matches 215; Conservative 0; Mismatches 174; Indels 3; Gaps 1;

QY 314 ctgacttctgacactgtgagacagagctgttctctgtaagcccaagtgtcaagcag 373
DB 417 CAGACTGGGTGATCCAGATCCAGAGAGAACCAAGCGCAAGCAAGAGGCGCCAG 476
QY 374 atgaggaagtgtgaggtcccaaatctgctgtatgtgaggaagagccatgtctac 433
DB 477 CCCCCAATGCTGGGCCAGAGCTTTCGCTGTCTGTGGGGAAGAGCCCTCCGGCTTC 536
QY 434 actcaatgcatgacatgtgagatgcaagagcttcttcaaggagggccatgaaagcga 493
DB 537 ACTCAAGTGTCTGACGTGCGAAGGCTGCAAGGGCTTTCGCGCGAGTGTGTCGCTG 596
QY 494 acgcccgtgtgaggttcccttcggaagggc---cctgtgatatcccccgaagccc 550
DB 597 GTGGGGCCAGGGGCTATGCTGCGGGGTGGGGAACCTGCAAGATGAGCCCTTCATGC 656
QY 551 gggcagctgtgcaagcctgctgcaagtgctgtgagagcggtcgtgaaagagaga 610
DB 657 GCGCGAAGTGCAGCAGATGCGCGCTGCGCAAGTGCAGAGGAGGAGGAGGAGCAGT 716
QY 611 tgatcatgtccgacgagcgctgtgagagagcggtgacctgatacagcggaagaaagt 670
DB 717 GCGTCTTTTGAAGAACAGATCCGGAAGAGAAAGATTCGGAACACAGCAGCAGAGT 776
QY 671 aagcgacggagctcagccactgtgagtgccag 702
DB 777 CACAGTCAAGTCCGAGTCACTGTGGGGCCG 808

RESULT 14
PCT-US94-12883-3

; Sequence 3, Application PC/TUS9412883
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR: COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas

COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12883
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152,003
FILING DATE: 10-NOV-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BARBARA S. KITCHELL
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD154P--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1813 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-12883-3

Query Match 3.3%; Score 97.2; DB 4; Length 1813;
Best Local Similarity 58.8%; Pred. No. 8.3e-13;
Matches 187; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 388 gtccccaatctgctgtatgtgagcaagcgccactgtctatcacttaatgtcaty 447
DB 229 GCGCAGAGCTTGGCGGTCTGTGTGGGACAGGCTTCGCGCTTCATACAGTGTCTC 288
QY 448 acatgtgaagatgcaagagcttcttcaaggagggccatgaaagcgaagcccgctgagg 507
DB 289 AGCTGGAGAGGCTGCAAGGCTTTCGCGCGCAAGTGTGCTGCGGCGCAGGCGC 348
QY 508 tgccttcggaagggc---cctgtgatatcccccgaagcccgaagcccgagtgccag 564
DB 349 TATGCTGCGGGGTGCGCAAGCTGCGCAAGTGTGAGGAGCTTTCATGCGCGCAAGTGCAG 408
QY 565 gcttcgctgtgcaagagtgctgtgagagcggtcgtgaaagagagatgatagtccgac 624
DB 409 CAGTGGCGGCTGCGCAAGTGTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 468
QY 625 gaagcgtgtgagagagcggtgctgtatcaagcggaagaaagtgaacggaagagact 684
DB 469 GAGCAGATCCGGAAGAGATTCGGAACACAGCAGCAGAGTCAAGTCAAGTCAAGTCA 528
QY 685 cagccactgtgagtgccag 702
DB 529 CAGTCAAGTGTGGGGCCG 546

RESULT 15

US-08-095-728B-3
; Sequence 3, Application US/08095728B
; Patent No. 5843642
; GENERAL INFORMATION:
; APPLICANT: DMITROVSKY, ETHAN
; APPLICANT: MARRELL JR, RAYMOND P
; APPLICANT: MILLER JR, WILSON H
; APPLICANT: FRANKEL, STANLEY
; TITLE OF INVENTION: METHODS FOR THE DETECTION AND

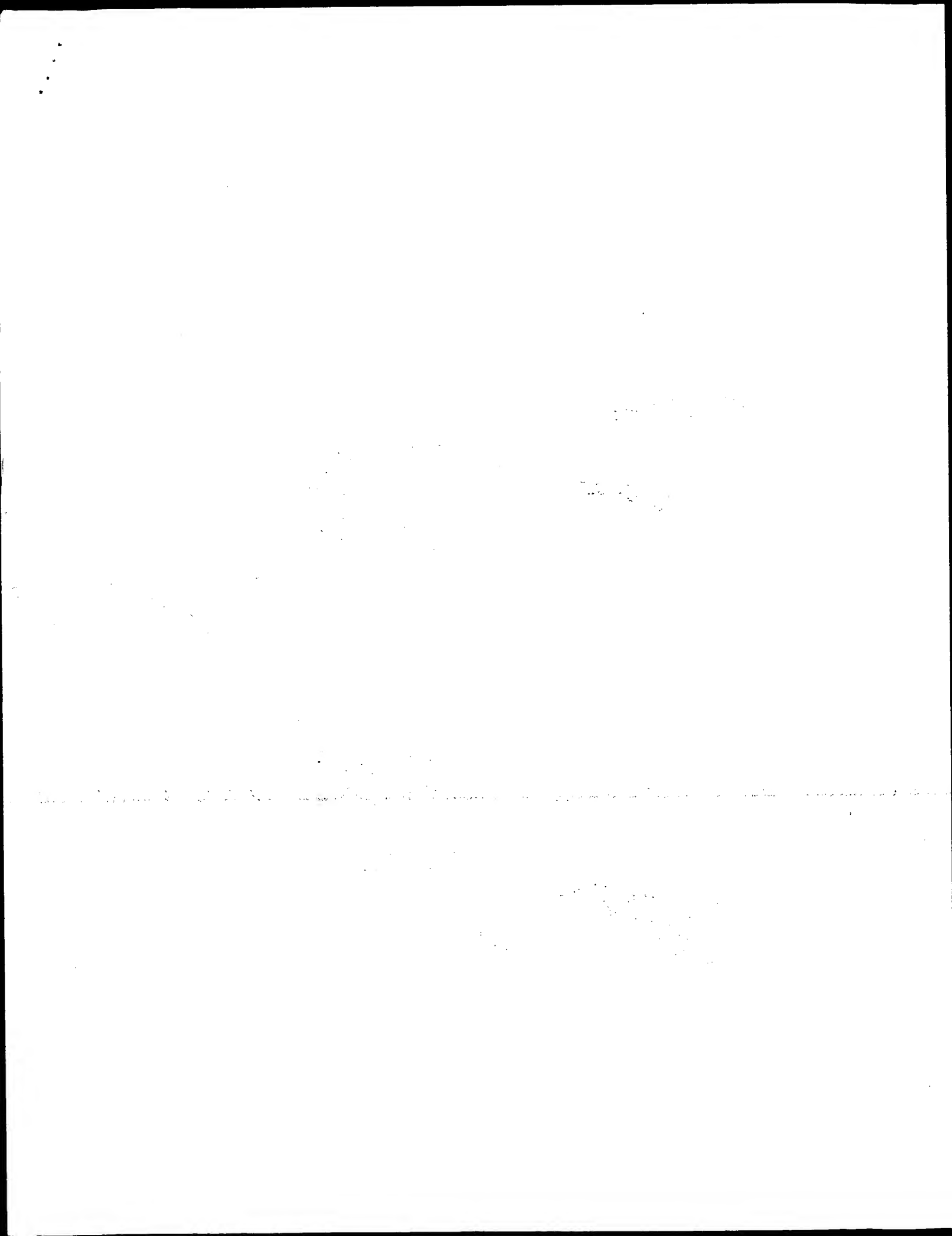
TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS: 11
 ADDRESSEE: COOPER & DUNHAM LLP
 STREET: 1185 AVENUE OF THE AMERICAS
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/095,728B
 FILING DATE: 21-JUL-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/673,838
 FILING DATE: 22-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: WHITE, JOHN P
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 38694-A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2928 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 IMMEDIATE SOURCE:
 CLONE: hRAR ALPHA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 103..1488
 OTHER INFORMATION:
 US-08-095-728B-3

Query Match 3.1%; Score 91.4; DB 2; Length 2928;
 Best Local Similarity 50.8%; Pred. No. 2e-11;
 Matches 302; Conservative 0; Mismatches 281; Indels 12; Gaps 3;

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 QY 1053 caaagtcattctcctacttcaggagacttgcacatcgagagacagatctccctgtgagg 1112
 DB 831 CAAGCAGCTGCCGGCTTACCAACCTCACCATCGCCGACCAAGATCACTCTCTCAAGGC 890
 QY 1113 ggcgcgttcgagctgtgtcaactgagatcaaacacagtgttcaacgcgagagactggaac 1172
 DB 891 TGCCTGCTGGACATCTGATCTCTGGGATCTGCACGCGGTACACGCCGAGAGAGACAC 950
 QY 1173 ctggagagtggt---ggcgcgctgtcctcactgcttgagagacactgcagtggtctcaga 1229
 DB 951 CATGACCTTCTCGAGAGGGCTGACCTGAACCGGACCAAGATGCACACGCTGGCTTCGG 1010
 QY 1230 acttctactgagagccatctgnaattccactacatcattgctgaaagagctgcaagctgcatga 1289
 DB 1011 CCCCTACACGACCTGCTCTTTCCTTTCGCAACGAGTGTGCTGCCCTGAGATGAGATA 1070
 QY 1290 gggaggtatgtgtatgcatgagagcattccctctctctccagagacgcccagtggtgct 1349
 DB 1071 TGGGGAGAGGGGGCTGCTACGCGCATCTGCTCATCTGCGAGACCGCCAGACCTTGA 1130
 QY 1350 ggaagcagcggtgtgtgacagctgcaagagacattcgcattactcgtgaagtcctact 1409

DB 1131 GCAGCCGAGACCGGTTGACATCTCTCAGAGCCGCTGCTGAGAGGGCTTAAGTTACT 1190
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 DB 1191 GCGGAAGCGAGCCCGCCGCCACCA-----TGTCCCAAGATGCTAATGAAGAT 1244
 QY 1470 caccgagctcgcagacatcattatgctcagacacacccagcgctgct---ggcattcaga 1526
 DB 1245 TACTGACTCTGCAGAGCATCAGCGCCAGAGGGGCTGAGGGGTGATCAGCTGAAGATGA 1304
 QY 1527 catcaccccttgcacgcccccatcagcagagtggttcgcatcacaggtagc 1581
 DB 1305 GATCCCGGGCTCCATGCGGCTCTCATCAGGAATGTTGAGAACTCAGAGGGC 1359

Search completed: February 18, 2001, 16:49:16
 Job time: 8375 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2001, 14:32:00 ; Search time 211.71 Seconds

(Without alignments)
5154.693 Million cell updates/sec

Title: US-09-143-828-1

Perfect score: 2905
Sequence: 1 cctctgaaggtcttagatc.....aaaaaaaaaaaaaaaaa 2905

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq_36:*

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21: /cgn2_2/gcgdata/geneseq/geneseq/NA2000.DAT:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2894	99.6	2910	20	X56242 Human vitamin D re
2	2804.6	96.5	3093	20	X78807 Human nmr7 cdna.
3	2804.2	96.5	3057	20	X59975 DNA encoding an in
4	2665.2	91.8	3243	20	X59974 DNA encoding an in
5	2651.2	91.3	2802	20	X56243 Human vitamin D re
6	2586.2	89.0	2850	20	X78808 Human nmr7-1 cdna.
7	2086.2	71.8	2146	20	X207997 Human pregnane x r
8	1686.2	58.0	2068	20	X89080 Human steroid and
9	1374	47.3	1374	20	X59967 DNA encoding an in
10	1330.2	45.8	1422	20	X59968 DNA encoding an in
11	1305	44.9	1305	20	X59966 DNA encoding an in
12	606.6	20.9	644	20	X59972 SEQ ID 12 of JP111

13	278.8	9.6	1960	19	V03129	CDNA encoding rat
14	278.8 <th>9.6</th> <td>2043</td> <td>14</td> <td>O51425</td> <td>Rat vitamin D rece</td>	9.6	2043	14	O51425	Rat vitamin D rece
15	272.8 <th>9.4</th> <td>1382</td> <td>20</td> <td>X34789</td> <td>Nucleotide sequenc</td>	9.4	1382	20	X34789	Nucleotide sequenc
16	272.8 <th>9.4</th> <td>1463</td> <td>20</td> <td>X34788</td> <td>Nucleotide sequenc</td>	9.4	1463	20	X34788	Nucleotide sequenc
17	272.8 <th>9.4</th> <td>1574</td> <td>20</td> <td>X34793</td> <td>Nucleotide sequenc</td>	9.4	1574	20	X34793	Nucleotide sequenc
18	272.8 <th>9.4</th> <td>3510</td> <td>20</td> <td>Z07545</td> <td>Human vitamin D re</td>	9.4	3510	20	Z07545	Human vitamin D re
19	272.8 <th>9.4</th> <td>4604</td> <td>19</td> <td>V41327</td> <td>Human vitamin D re</td>	9.4	4604	19	V41327	Human vitamin D re
20	271.2 <th>9.3</th> <td>1399</td> <td>14</td> <td>O51424</td> <td>Human vitamin D re</td>	9.3	1399	14	O51424	Human vitamin D re
21	257 <th>8.8</th> <td>2191</td> <td>17</td> <td>T36499</td> <td>Xenopus orphan rec</td>	8.8	2191	17	T36499	Xenopus orphan rec
22	236 <th>8.1</th> <td>1071</td> <td>20</td> <td>X16596</td> <td>Rat vitamin D rece</td>	8.1	1071	20	X16596	Rat vitamin D rece
23	236 <th>8.1</th> <td>3382</td> <td>19</td> <td>V18518</td> <td>CDNA encoding rat</td>	8.1	3382	19	V18518	CDNA encoding rat
24	236 <th>8.1</th> <td>3382</td> <td>20</td> <td>X16606</td> <td>Rat vitamin D rece</td>	8.1	3382	20	X16606	Rat vitamin D rece
25	215 <th>7.4</th> <td>1534</td> <td>20</td> <td>X34790</td> <td>Nucleotide sequenc</td>	7.4	1534	20	X34790	Nucleotide sequenc
26	188.6 <th>6.5</th> <td>1404</td> <td>20</td> <td>X16597</td> <td>Human vitamin D re</td>	6.5	1404	20	X16597	Human vitamin D re
27	185.4 <th>6.4</th> <td>1404</td> <td>19</td> <td>V03130</td> <td>CDNA encoding rat</td>	6.4	1404	19	V03130	CDNA encoding rat
28	181.6 <th>6.3</th> <td>1280</td> <td>20</td> <td>X80215</td> <td>Mouse nuclear rece</td>	6.3	1280	20	X80215	Mouse nuclear rece
29	172.2 <th>5.9</th> <td>1450</td> <td>18</td> <td>T92305</td> <td>Constitutively act</td>	5.9	1450	18	T92305	Constitutively act
30	170.6 <th>5.9</th> <td>1450</td> <td>14</td> <td>O46131</td> <td>Human CAR receptor</td>	5.9	1450	14	O46131	Human CAR receptor
31	170.6 <th>5.9</th> <td>1450</td> <td>20</td> <td>X23994</td> <td>Human CAR receptor</td>	5.9	1450	20	X23994	Human CAR receptor
32	168.6 <th>5.8</th> <td>1361</td> <td>20</td> <td>X24003</td> <td>Mouse CAR receptor</td>	5.8	1361	20	X24003	Mouse CAR receptor
33	108.4 <th>3.7</th> <td>468</td> <td>20</td> <td>X80217</td> <td>Mouse nuclear rece</td>	3.7	468	20	X80217	Mouse nuclear rece
34	97.6 <th>3.4</th> <td>1898</td> <td>18</td> <td>T79634</td> <td>DNA encoding human</td>	3.4	1898	18	T79634	DNA encoding human
35	97.6 <th>3.4</th> <td>1979</td> <td>17</td> <td>T27616</td> <td>Human foetal lung</td>	3.4	1979	17	T27616	Human foetal lung
36	97.6 <th>3.4</th> <td>2030</td> <td>15</td> <td>O63134</td> <td>Human recombinant</td>	3.4	2030	15	O63134	Human recombinant
37	97.6 <th>3.4</th> <td>2030</td> <td>17</td> <td>T18996</td> <td>Human steroid rece</td>	3.4	2030	17	T18996	Human steroid rece
38	97.6 <th>3.4</th> <td>2030</td> <td>17</td> <td>T30031</td> <td>NER receptor poten</td>	3.4	2030	17	T30031	NER receptor poten
39	97.2 <th>3.3</th> <td>1813</td> <td>16</td> <td>O88760</td> <td>Human ubiquitouse n</td>	3.3	1813	16	O88760	Human ubiquitouse n
40	91.4 <th>3.1</th> <td>2928</td> <td>13</td> <td>O29338</td> <td>Human RAR-alpha gene</td>	3.1	2928	13	O29338	Human RAR-alpha gene
41	91.4 <th>3.1</th> <td>2928</td> <td>20</td> <td>V64991</td> <td>Human RAR-alpha cd</td>	3.1	2928	20	V64991	Human RAR-alpha cd
42	91.4 <th>3.1</th> <td>2940</td> <td>10</td> <td>N90124</td> <td>DNA of clone pRAR</td>	3.1	2940	10	N90124	DNA of clone pRAR
43	91.4 <th>3.1</th> <td>3036</td> <td>13</td> <td>O29334</td> <td>myl/RAR-alpha fusi</td>	3.1	3036	13	O29334	myl/RAR-alpha fusi
44	91.4 <th>3.1</th> <td>3036</td> <td>19</td> <td>V20474</td> <td>Human PML/RARalpha</td>	3.1	3036	19	V20474	Human PML/RARalpha
45	91.4 <th>3.1</th> <td>3036</td> <td>20</td> <td>V64990</td> <td>Human myl/RAR-alpha</td>	3.1	3036	20	V64990	Human myl/RAR-alpha

ALIGNMENTS

RESULT 1
ID X56242 standard; CDNA: 2910 BP.
AC X56242;
DT 16-JUL-1999 (first entry)
XX
DE Human vitamin D receptor related gamma protein encoding CDNA.
XX
KW Human; vitamin D receptor related protein; VDR; obesity; diabetes;
KW anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia;
KW hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; tumour;
KW hyperproliferative skin disorder; hyperthyroidism; ss.
XX
OS Homo sapiens.
XX
PN WO9919354-A1.
XX
PD 22-APR-1999.
XX
PF 31-AUG-1998; 98WO-SE01548.
XX
PR 31-MAR-1998; 98SE-0001148.
PR 14-OCT-1997; 97SE-0003745.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Berkenstam A, Dahlberg M;
XX
XX WPI: 1999-302508/25.
XX P-PSDB; Y09515.
XX
XX New vitamin D receptor related (VDR) polypeptides, useful for
XX treating obesity, diabetes, anorexia and rheumatoid arthritis
XX
XX

Db 234 tccgtaacagcagcgcctctctgttaagctactcctgatcgatcctcttgacccgga 293
QY 202 ttgttccaagtggagcccaaggagagatcggagcaagaacttaccaccaagacgtcca 261
Db 294 ttgttccaagtggagcccaaggagagatcggagcaagaacttaccaccaagacgtcca 353
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Db 414 gtacacgtggagagacagagatcgttctcgtgaaagcccaagtgtcaacagatgagaa 473
QY 382 gtccgagagctcccaaaatctccgctgtatgtggagcaagaagcccaagtgtatcaat 441
Db 474 gtccgagagctcccaaaatctccgctgtatgtggagcaagaagcccaagtgtatcaat 533
QY 442 gtcatgacatgtgaagagatgcgaagagctttctcagagagcccatgaaacgcaagcccg 501
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Db 654 cagagctgcgcgcctgcggaagagctgcggaagagcgcccatgaaagagagatgatactc 713
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Db 1494 tccatcatgagatgcaatcgccccaagcgtctcataggtctctgttctctgaaagatcag 1553
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Db 1674 tgaagcgctgacccctgggtgagacactccgagagcgagcccaagacccctctgagcc 1733
QY 1642 gccaccccggtgcgaagagatgagacactgcgcaagagccgacaaatgcccgtctgagcc 1701
Db 1734 gccaccccggtgcgaagagatgagacactgcgcaagagccgacaaatgcccgtctgagcc 1793
QY 1702 tctccctaagggaatctctgctatgacagctggctgacatctcctcagagagagacatgag 1761
Db 1794 tctccctaagggaatctctgctatgacagctggctgacatctcctcagagagagacatgag 1853
QY 1762 ccccccaccccaagctcagctgtgtagagagtgagacacagactctcagtgagagtgcc 1821
Db 1854 ccccccaccccaagctcagctgtgtagagagtgagacacagactctcagtgagagtgcc 1913
QY 1822 actgacactgtgaagtgagagccatcagagagagagaggttgcccttctcttaaaagcgcc 1881
Db 1914 actgacactgtgaagtgagagccatcagagagagagaggttgcccttctcttaaaagcgcc 1973
QY 1882 tgtgtgctggagagaaatccctcagagatcccaactaaagtgtgcaaggtgtgagagagccaa 1941
Db 1974 tgtgtgctggagagaaatccctcagagatcccaactaaagtgtgcaaggtgtgagagagccaa 2033
QY 1942 gggaccaaagatagagccatctgggtgtctatgcccacatacccaagttgttcgctcctg 2001
Db 2034 gggaccaaagatagagccatctgggtgtctatgcccacatacccaagttgttcgctcctg 2093
QY 2002 agtctttcatgtgacacttaagtctcgtctcccaactcccaactgcttccctccctc 2061
Db 2094 agtctttcatgtgacacttaagtctcgtctcccaactcccaactgcttccctccctc 2153
QY 2062 ttccagagctgcttggtggctcaaaagcgtgtactcatctgcgaggtgcatgtgatactg 2121
Db 2154 ttccagagctgcttggtggctcaaaagcgtgtactcatctgcgaggtgcatgtgatactg 2213
QY 2122 ggaagctcttaagagagatgagagccagagagcgtgcacccaatgtcgaagagcttgagat 2181
Db 2214 ggaagctcttaagagagatgagagccagagagcgtgcacccaatgtcgaagagcttgagat 2273
QY 2182 gaaactatctcggagacacatctcgtgtctctgataccatgttgaaacatattaaagca 2241
Db 2274 gaaactatctcggagacacatctcgtgtctctgataccatgttgaaacatattaaagca 2333
QY 2242 ctgatataggtagagcgtctggtgggtatacagacatgactcagatatagatctcagact 2301
Db 2334 cagataaatgtgagagcgtctggtgggtatacagacatgactcagatatagatctcagact 2393
QY 2302 cacaagatttaagttaaaaaaacaagaagaacaacaatttgatcaaaagagaa 2361
Db 2394 cacaagatttaagttaaaaaaacaagaagaacaacaatttgatcaaaagag-a 2452

QY 1628 gaagccctctgagccgacactcccgagccaagacagatgacactgccaaagccgacaat 1687
 DB 1809 gagccctctgagccgacactcccgagccaagacagatgacactgccaaagccgacaat 1868
 QY 1688 gccctctgagccctgctccctagaggaatctctgctatagacaagctggtacatctccag 1747
 DB 1869 gccctctgagccctgctccctagaggaatctctgctatagacaagctggtacatctccag 1928
 QY 1748 gaagagcattggtgcccccccccaagttcagctctgtatggaggtggaagcccaactct 1807
 DB 1929 gaagagcattggtgcccccccccaagttcagctctgtatggaggtggaagcccaactct 1988
 QY 1808 tacgtgagagtgacactgacactctgtatgagacacatccagaaagccaaagttgccccttc 1867
 DB 1989 tacgtgagagtgacactgacactctgtatgagacacatccagaaagccaaagttgccccttc 2048
 QY 1868 cttttaaagagccctgtggtctgtggtggaatccctcagatcccaataaagtgtcaagt 1927
 DB 2049 cttttaaagagccctgtggtctgtggtggaatccctcagatcccaataaagtgtcaagt 2108
 QY 1928 gttggaagggacacagccacgaagataagccactgtggtgtctatgtcccaatacccaagt 1987
 DB 2109 gttggaagggacacagccacgaagataagccactgtggtgtctatgtcccaatacccaagt 2168
 QY 1988 ttgttgcctctgagctcttccatctgacactcctaatagtctctgtcccaactccac 2047
 DB 2169 ttgttgcctctgagctcttccatctgacactcctaatagtctctgtcccaactccac 2228
 QY 2048 tctgtccctctctctcagagctgtctgtggtggtcacaagccctgactcactccgaggtg 2107
 DB 2229 tctgtccctctctctcagagctgtctgtggtggtcacaagccctgactcactccgaggtg 2288
 QY 2108 catgagatctgtgtggaggtccctctagagagatgagaagccaaagccctgacccaagt 2167
 DB 2289 catgagatctgtgtggaggtccctctagagagatgagaagccaaagccctgacccaagt 2348
 QY 2168 cagaagcttgagatgacactcactccgacacatctctgtctgtcctgcatcatttga 2227
 DB 2349 cagaagcttgagatgacactcactccgacacatctctgtctgtcctgcatcatttga 2408
 QY 2228 cacatattaaagcactgataatagtagtctgtgtggtgtatatacagattgactcagat 2287
 DB 2409 cacatattaaagcactgataatagtagtctgtgtggtgtatatacagattgactcagat 2468
 QY 2288 atagatcctgagctcagcagagtttatagttaaaaaacaacagaacacaaacatttg 2347
 DB 2469 atagatcctgagctcagcagagtttatagttaaaaaacaacagaacacaaacatttg 2528
 QY 2348 gatcaaaaggaataatgatagtacaaaagcagacaaaggaattccctgtgtgaggtg 2407
 DB 2529 gatcaaaaggaataatgatagtacaaaagcagacaaaggaattccctgtgtgaggtg 2587
 QY 2408 ctgagctgtgatagtcagcagctgtgtgtacccaagtgaaggtcccgagagacatgagctgt 2467
 DB 2588 ctgagctgtgatagtcagcagctgtgtgtacccaagtgaaggtcccgagagacatgagctgt 2647
 QY 2468 aggaagaagggaacaaactgcagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2527
 DB 2648 aggaagaagggaacaaactgcagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2707
 QY 2528 tctttgcccactgtatgggggcccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2587
 DB 2708 tctttgcccactgtatgggggcccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2767
 QY 2588 tgacaaggtctacgtcgtgaacatcagttaaacacacgcggaagaacacattatcatgcaact 2647
 DB 2768 tgacaaggtctacgtcgtgaacatcagttaaacacacgcggaagaacacattatcatgcaact 2827
 QY 2648 tataattctgtgtacacatctatctcaaaagtaaggtatgaaggtgctgtgtgtgtgtgtgtgt 2707
 DB 2828 tataattctgtgtacacatctatctcaaaagtaaggtatgaaggtgctgtgtgtgtgtgtgtgt 2887

QY 2708 tatagccactgtgagtaaaatatttttgcattttcacaaatatactattatagaagc 2767
 DB 2888 tatagccactgtgagtaaaatatttttgcattttcacaaatatactattatagaagc 2947
 QY 2768 attcacacctaagaagtaatttttgggaatgtagccctgtgtgtgtgtgtgtgtgtgtgtgt 2827
 DB 2948 attcacacctaagaagtaatttttgggaatgtagccctgtgtgtgtgtgtgtgtgtgtgtgt 3007
 QY 2828 caaaaggaattaaataatgacttttggctaaa 2860
 DB 3008 caaaaggaattaaataatgacttttggctaaa 3040

RESULT 5

ID X56243 standard; cDNA; 2802 BP.
 AC X56243;
 XX
 XX
 DT 16-JUL-1999 (first entry)
 XX

DE Human vitamin D receptor related gamma 2 protein encoding cDNA.

XX Human; vitamin D receptor related protein; VDR; obesity; diabetes;
 KW anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia;
 KW hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; tumour;
 KW hyperproliferative skin disorder; hyperthyroidism; ss.
 XX

OS Homo sapiens.

PN WO9919354-A1.

PD 22-APR-1999.

PF 31-APR-1998; 98MO-SE01548.

PR 31-MAR-1998; 98SE-0001148.

PR 14-OCT-1997; 97SE-0003745.

PA (PHMA) PHARMACIA & UPJOHN AB.

PI Berkenstam A, Dahlberg M;

WP1: 1999-302508/25.

P-P-SDB; Y09516.

XX New vitamin D receptor related (VDR) polypeptides, useful for

XX treating obesity, diabetes, anorexia and rheumatoid arthritis

XX Claim 2; Page 21-22; 35pp; English.

CC The present sequence encodes a human vitamin D receptor related (VDR)
 CC polypeptide. Human VDR polypeptides and substances which affect VDR
 CC signal transduction, can be used for treating metabolic, proliferative
 CC or inflammatory conditions. They can be used in the manufacture of a
 CC medicament for treating the following conditions: obesity, diabetes,
 CC anorexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or
 CC hyperlipoproteinaemia and osteoporosis, rheumatoid arthritis, benign and
 CC malignant tumours, hyperproliferative skin disorders or hyperthyroidism.
 CC Nucleic acid vectors encoding for expression of a VDR polypeptide can
 CC be used for treating metabolic, proliferative or inflammatory conditions,
 CC by introducing them into a mammal. The introduced nucleic acid is then
 CC capable of transforming a cell in vivo and then polypeptide is expressed.
 CC A substance affecting VDR signal transduction, such as an agonist or
 CC antagonist can be used for the manufacture of a medicament for treating
 CC metabolic, proliferative or inflammatory condition.
 CC N.B. The specification specifically claims the VDR nucleic acid and
 CC polypeptide sequences given in figures 1, 4, 7 and 8, but no figures
 CC are given in the specification.

SQ Sequence 2802 BP; 723 A; 715 C; 755 G; 609 T; 0 other;

[illegible][illegible]


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DB 1720 ggcctctccctcaggaattcctctcgtacagcgtgctagcattcctccaggaagaca 1779
QY 1756 tgggtgccccccaccccgctcagctctgttagagagtagaagccacagactcttaagtga 1815
DB 1780 tgggtgccccccaccccgctcagctctgttagagagtagaagccacagactcttaagtga 1839
QY 1816 ggtgctacgtacgtctaggtcagacacatcagaagagcaaggttgccttctcttaaa 1875
DB 1840 ggtgctacgtacgtctaggtcagacacatcagaagagcaaggttgccttctcttaaa 1899
QY 1876 aggcctctgtgtctgtgggagaaatccctcagaatcccaataaagtctcaaggtgtgaaag 1935
DB 1900 aggcctctgtgtctgtgggagaaatccctcagaatcccaataaagtctcaaggtgtgaaag 1959
QY 1936 gaccagagacacaaagatagagcactgtgtgtctatgccccacataccagttgttcgc 1995
DB 1960 gaccagagacacaaagatagagcactgtgtgtctatgccccacataccagttgttcgc 2019
QY 1996 ttccctgagcttttctatgtctacccataagctctgtctccacttccactgttcgc 2055
DB 2020 ttccctgagcttttctatgtctacccataagctctgtctccacttccactgttcgc 2079
QY 2056 ctctctctccagagctgtctgtgtggctcaagagcctgtactcagcagagtgatagta 2115
DB 2080 ctctctctccagagctgtctgtgtggctcaagagcctgtactcagcagagtgatagta 2139
QY 2116 tctgtgg 2122
DB 2140 tctgtgg 2146

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RESULT 8

X89080
ID X89080 standard; DNA; 2068 BP.

XX X89080;

DT 14-SEP-1999 (first entry)

DE Human steroid and xenobiotic receptor (SXR) encoding DNA.

XX Nuclear receptor; SXR; steroid and xenobiotic receptor; RXR; human;
 KW retinoid X receptor; P450 gene; steroid hormone; steroid metabolism;
 KW phytoestrogen; calcium-channel blocker; steroid toxicity; tuberculosis;
 KW breast cancer; osteoporosis; Cushing syndrome; vitilism; hirsutism;
 KW polycystic ovarian disease; cancer; colorectal; prostatic; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 583..1887

XX FT /*tag= a /transl_except= (pos:1261..1263, aa:Xaa)

XX FT /note= "Xaa= unknown; the start codon is not indicated"

XX PN M09935246-A1.

XX PD 15-JUL-1999.

XX PF 08-JAN-1999; 99WO-US00490.

XX PR 09-JAN-1998; 98US-0005286.

XX PA (SALK) SALK INST BIOLOGICAL STUDIES.

XX PI Blumberg B, Evans RM;

XX DR WPI; 1999-419349/35.

XX PT P-PSDB; Y21799.

PT New steroid and xenobiotic receptor, used to identify modulators for
 controlling metabolism of steroids and xenobiotics, e.g. reducing

PT their toxicity
 XX
 PS Claim 10; Fig 1A; 83pp; English.

CC The invention relates to a novel nuclear receptor polypeptide, designated
 CC SXR (steroid and xenobiotic receptor). SXR (1) forms a heterodimer with
 CC retinoid X receptor (RXR), (11) binds to a direct or inverted repeat
 CC response element motif based on the half-site AGTGA, (11) activates
 CC transcription through response elements present in steroid-inducible P450
 CC genes, in response to a wide variety of natural and synthetic steroid
 CC hormones and (1V) is prominently expressed in liver and intestine. SXR
 CC regulates expression of catabolic enzymes, in response to many different
 CC steroids, and thus affects metabolism. SXR is a broad specificity, low-
 CC affinity receptor for reducing excessive levels of steroids in the
 CC circulation. (Antagonists of SXR are used to regulate metabolism of
 CC steroids particularly phytoestrogens or calcium-channel blockers, to
 CC reduce steroid toxicity in subjects being treated with steroids, e.g. in
 CC cases of tuberculosis (treated with rifampin and related compounds),
 CC breast cancer (treated with tamoxifen, raloxifen etc.) or osteoporosis
 CC (treated with Vitamin K), or to slow metabolism of therapeutic steroids.
 CC Also, modulating endogenous SXR is used to treat disease, particularly
 CC an agonist is used where endogenous steroid levels are excessive (e.g.
 CC Cushing syndrome; vitilism and hirsutism in women; polycystic ovarian
 CC disease; 11 beta-, 17- or 21-hydroxylase deficiency; 3 beta-hydroxysteroid
 CC dehydrogenase deficiency, or breast, colorectal or prostatic cancer),
 CC while antagonists are used where endogenous steroid levels are too low.
 CC Cells that express SXR are used to identify compounds likely to be
 CC involved in undesirable drug interactions. Antibodies specific for SXR
 CC are used in immunohistochemical testing for studying distribution/
 CC expression density of SXR, also for diagnosis and therapeutically as
 CC antagonist. The present sequence represents the longest SXR cDNA clone
 CC encoding the SXR polypeptide.

SQ Sequence 2068 BP; 520 A; 541 C; 586 G; 420 T; 1 other;

Query Match 58.0%; Score 1686.2; DB 20; Length 2068;

Best Local Similarity 98.7%; Pred. No. 0;

Matches 1730; Conservative 0; Mismatches 19; Indels 3; Gaps 3;

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QY 16 gaatcagatgtaattcgttggacgggaagaggaagcactgccttactcagtggaaat 75
DB 319 gaatacatacctatgactagcagcggaagaggaagcactgccttactcagtggaaat 378
QY 76 ctggcctcagcttgtaagcagcaggtttcaacgtgtaaaagaaagaaagaaagaaagaa 135
DB 379 ctggcctcagccttgtaagcagcaggtttcaacgtgtaaaagaaagaaagaaagaaagaa 438
QY 136 ctctgtctgtaacaaagcagcgctccttggtaagcctacccctgatacgtatccttcgc 195
DB 439 ctctgtctcgaacaaagcagcgctccttggtaagcctacccctgatacgtatccttcgc 498
QY 196 accggaattgticaaagtggaccccaagggaagagtcgagcaaaagaaacttaccaacaagc 255
DB 499 accggaattgticaaagtggaccccaagggaagagtcgagcaaaagaaacttaccaacaagc 558
QY 256 agtccaagaagcccaagaacaaactggaggtgagagcccaagaagaagctggaaacatgct 315
DB 559 agtccaagaagcccaagaacaaactggaggtgagagcccaagaagaagctggaaacatgct 618
QY 316 gactttgtaactgttaggacacagagctgtctccctggaaagcccggttcaacgaagat 375
DB 619 gactttgtaactgttaggacacagagctgtctccctggaaagcccggttcaacgaagat 678
QY 376 gaggaaagtcggaagtcgcccaaatctgcgtgtatgtggggaacaagccctggctatcac 435
DB 679 gaggaaagtcggaagtcgcccaaatctgcgtgtatgtggggaacaagccctggctatcac 738
QY 436 ttaaatgtatgacatgtgtaagatcaagaaggtctttcaagagggccatgaagcaaac 495
DB 739 ttaaatgtatgacatgtgtaagatcaagaaggtctttcaagagggccatgaagcaaac 798
QY 496 gcccggtgagggtgcctctcggaaagggcgctgtagagatcacccggaaagcccgcgga 555

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[illegible]

Db	1261	accagagcccgagatataatgctcagacaccccgcgctgctgcattccaggaacta	1320
Qy	1511	cacccttgcctacgcccctcatgcagagatgtgttcggcatcacaggtacgtga	1584
Db	1321	cacccttgcctacgcccctcatgcagagatgtgttcggcatcacaggtacgtga	1374
RESULT	10		
XX	559968	standardc; DNA; 1422 BP.	
XX	AC	X559968;	
XX	DT	04-AUG-1999 (first entry)	
XX	DE	DNA encoding an intranuclear receptor protein.	
XX	KW	Human; intranuclear receptor protein; drug development; diagnosis;	
XX	OS	treatment; ss.	
XX	XX	Homo sapiens.	
XX	PN	JP11127872-A.	
XX	PD	18-MAY-1999.	
XX	PF	07-AUG-1998; 98JP-0224172.	
XX	PR	11-AUG-1997; 97JP-0230335.	
XX	PA	(NISB) JAPAN TOBACCO INC.	
XX	DR	WPI; 1999-350330/30.	
XX	DR	P-PSDB; Y15933.	
XX	PT	New intranuclear receptor protein - useful for drug development and	
XX	PT	diagnosis and treatment of disease	
XX	PS	Claim 4; Page 25-27; 38pp; Japanese.	
CC	CC	The present sequence encodes a human intranuclear receptor protein.	
CC	CC	The nucleic acid sequence was isolated from a human adult cDNA	
CC	CC	library using a swissalish ANO23 derived probe. The protein can	
CC	CC	be used for the development of drugs and diagnosis and treatment	
CC	CC	of various diseases.	
XX	XX	Sequence 1422 BP; 336 A; 395 C; 414 G; 277 T; 0 other:	
Qy	Query Match	45.8%; Score 1330.2; DB 20; length 1422;	
Db	Best Local Similarity	99.4%; Pred. No. 5.4e-263;	
XX	Matches 1335; Conservative	0; Mismatches 8; Indels 0; Gaps 0;	
Qy	242	acttccacacagcagcgtcccaagagggcccaagacgaacccctggaggttgagaccacaaagaa	301
Db	80	agttgcttccgaacacatccacagagggcccaagacgaacccctggaggttgagaccacaaagaa	139
Qy	302	gtctgagacacatgctctctcttgaacactgtgagagacacagatctcttctctgaaagccca	361
Db	140	gtctgagacacatgctctcttgaacactgtgagagacacagatctcttctctgaaagccca	199
Qy	362	gtgtcaacgcagatagagagagtcgagaggttcccaaatctgcgtgtatgtgagagcaag	421
Db	200	gtgtcaacgcagatagagagagtcgagaggttcccaaatctgcgtgtatgtgagagcaag	259
Qy	422	ccactggtatctacttcaatgtcatgtacaatgtgaagagatgcaagggcttttcagagag	481
Db	260	ccactggtatctacttcaatgtcatgtacaatgtgaagagatgcaagggcttttcagagag	319
Qy	482	ccatgaacgcagaccccggtgtaggtgtcccttcggagagggcgccgtcgagatcaccc	541
Db	320	ccatgaacgcagaccccggtgtaggtgtcccttcggagagggcgccgtcgagatcaccc	379

[illegible]

KM	Human: intranuclear receptor protein; drug development; diagnosis;
KW	treatment, ss.
XX	Homo sapiens.
OS	JF1127872-A.
PN	16-MAY-1999.
XX	
PD	07-AUG-1998; 98JP-0224172.
XX	
PF	11-AUG-1997; 97JP-0230335.
XX	
PA	(NINSB) JAPAN TOBACCO INC.
XX	
DR	WPJ; 1999-350330/30.
XX	
PT	New intranuclear receptor protein - useful for drug development and
PT	diagnosis and treatment of disease
XX	
PS	Disclosure; Page 32; 38pp; Japanese..
XX	
CC	The specification describes a human intranuclear receptor protein.
CC	The nucleic acid sequence was isolated from a human adult CDNA
CC	library using a swellfish ANO3 derived probe. The protein can
CC	be used for the development of drugs and diagnosis and treatment
CC	of various diseases. The present sequence was used in the course of
CC	the invention.
XX	
SQ	Sequence 644 BF; 175 A; 161 C; 193 G; 115 T; 0 other;
	Query Match 20.9%; Score 606.6; DB 20; Length 644;
	Best Local Similarity 99.2%; Pred.No. 3,1e-115;
	Matches 620; Conservative 0; Mismatches 4; Indels 1; Gaps 1.
OY	55 tgccttacttcgtggaatcctcgctccagctcgcaagcagtgttaacagtgaataa 114
DB	12 tgcctttacttcagtgattcgttcggctccagctcgcaagtggttacaggtgaaga 70
OY	115 aaagaagaagataagataactacctgctcctaacaaggcagcgctccctgtgaagct 174
DB	71 aagaagaagaataagataactatactctgtccctgaaaaaagcgcgctccctgtgtaaagct 130
OY	175 actccttgatcgatctccttctgcaccggatgtgttcaaatgtgaaccccagggagaaagtcgga 234
DB	131 actccttgatcgatctccttctgcaccggatgtgttcaaatgtgaaccccagggagaaagtcgga 190
OY	235 gcaaaagaacttaccaccaagcagctccaagaagccccagaagaaccccgagggtgaagcccc 284
DB	191 gcaaaagaacttaccaccaagcagctccaagaagccccagaagaaccccgagggtgaagcccc 250
OY	295 aaaagaagcctggagaaccatctgaacttctgaacactgtgaagacacagaaggtcgtgtcccgga 354
DB	251 aaaagaagcctggagaaccatctgaacttctgaacactgtgaagacacagaaggtcgtgtcccgga 310
OY	355 aagcccgatgttcaaagcgcaagatgaaggaagtcgggaaggtccccaatatctgcgttgtatgtggg 414
DB	311 aagcccgatgttcaaagcgcaagatgaaggaagtcgggaaggtccccaatatctgcgttgtatgtggg 370
OY	415 gacaagaagcaccttgcttatcaacttcaatgatcatgatgacatgtgaagaatgcaaaaggtcttttc 474
DB	371 gacaagaagcaccttgcttatcaacttcaatgatcatgatgacatgtgaagaatgcaaaaggtcttttc 430
OY	475 aggaagggccatgtgaagaagcacaagcccgagctggaaggtgcccttcctcggaagggcgcttggaag 534
DB	431 aggaagggccatgtgaagaagcacaagcccgagctggaaggtgcccttcctcggaagggcgcttggaag 490
OY	535 atccacccggagaagcccgcgacagatgtgcacagcgcttcgcgcctgcgcaaggtgccttggaagagc 594
DB	491 atccacccggagaagcccgcgacagatgtgcacagcgcttcgcgcctgcgcaaggtgccttggaagagc 550
OY	555 ggcactgaagaagaagatgatcatgatctgcgaagagccgctgtgaaggaagggcgggccttgatc 654

OS1425
ID OS1425 standard; cDNA; 2043 BP.
XX
AC OS1425;
XX
DT 16-MAY-1994 (first entry)
XX
DE Rat vitamin D receptor coding sequence.
XX
KW 1,25-dihydroxyvitamin D3 receptor; recombinant protein production;
XX Insect host; ds.
OS Rattus rattus.
XX
FH Key Location/Qualifiers
FT mat_peptide 266..1363
FT /tag= a
FT /product= vitamin_D_receptor
XX
PN US5260199-A.
XX
PD 09-NOV-1993.
XX
PE 30-JUL-1991; 91US-0737736.
XX
PR 30-JUL-1991; 91US-0737736.
XX
PA (MISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Deluca HF, Prahil JM, Ross TK;
XX
DR WPI, 1993-367874/46.
DR P-PSDB; R43656.
XX
PT Recombinant prodn. of 1,25-dihydroxy-vitamin-D3 receptor protein
PT - using expression system comprising insect cell host and
PT recombinant virus contg. foreign DNA
XX
PS Disclosure; Columns 15-18; 13pp; English.
XX
CC The 1,25-dihydroxyvitamin D3 receptor is recombinantly produced
CC using insect host cells transformed with DNA coding for an animal
CC (prof. human, rat, porcine or avian) vitamin D receptor. The coding
CC sequence is incorporated into a recombinant baculovirus vector for
CC transformation of the insect host. The rat version of the coding
CC sequence was published in Burmester et al., Proc.Natl. Acad. Sci USA
CC 85:9499-9502 (1988).
XX
SO Sequence 2043 BP; 448 A; 647 C; 518 G; 430 T; 0 other;

Query Match 9.6%; Score 278.8; DB 14; Length 2043;
Best Local Similarity 55.6%; Pred. No. 4,1e-48;
Matches 629; Conservative 0; Mismatches 482; Indels 21; Gaps 4;

DB 391 ccccaaatgctgctgtagtggaggaagccatgctctatcattcaatgtcatgaca 450
DB 155 ccccgagctctgtgagtggtgagacgagccagctctccattcaatgtcatgacc 214
DB 451 tctgagaggtgcaagggtcttttcagagaggtgcatgaaacgacagcccgctgaggtgc 510
DB 215 tctgagaggtgcaagggtctcttcagagcagagcatgaaagcgagaggtcttcacctgt 274
DB 511 cccctccgagagggcgctgctgagacacacgagagacccgagcagagtcgagcctgc 570
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RESULT 15
X34789
ID X34789 standard; DNA; 1382 BP.
XX
AC X34789;
XX
DT 06-JUL-1999 (first entry)
XX
DE Nucleotide sequence of human vitamin D receptor (VDR) gene transcript 9.
XX
KW Vitamin D receptor; VDR; hVDR; variant; isoform; SRC-1; GRIP-1; TRTB;
XX cofactor; human; ds.
OS Homo sapiens.

XX WO9916872-A1.
 XX 08-APR-1999.
 XX 29-SEP-1998; 98WO-AU00817.
 XX 29-SEP-1997; 97AD-0009500.
 XX (GARV-) GARVAN INST MEDICAL RES.
 XX Crofts LA, Eisman JA, Hancock MS, Morrison NA;
 XX WPI, 1999-263693/22.
 XX P-PSDB; Y09036.

XX New polynucleotides which encode novel isoforms of the human vitamin
 PT D receptor or variant transcripts for hvDR
 PS Claim 4; Fig 6; 56pp; English.

XX The invention relates to isolated polynucleotides which encode novel
 CC isoforms of the human vitamin D receptor (VDR) or variant transcripts for
 CC hvDR. The polynucleotides are useful in methods for detecting agonist and
 CC /or antagonist compound of a VDR isoform. An increase or decrease in
 CC activity of the receptor may be detected by measuring changes in
 CC interactions with known cofactors (e.g. SRC-1, GRIP-1 and TRIP1B) or
 CC unknown cofactors (e.g. through use of the dual hybrid system). The
 CC polynucleotides shown in X34787, X34791 and X34792 (corresponding to
 CC hvDR exon sequences) may be useful as probes for the detection of VDR
 CC variant transcripts and for assessing cell or tissue-specific expression
 CC of variant transcripts. The present sequence represents the nucleotide
 CC sequence of hvDR gene transcript 9.

XX Sequence 1382 BP; 310 A; 409 C; 379 G; 284 T; 0 other;

Query Match 9.4%; Score 272.8; DB 20; Length 1382;

Best Local Similarity 55.1%; Pred. NO. 6.2e-47;
 Matches 638; Conservative 0; Mismatches 487; Indels 33; Gaps 4;

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Search completed: February 18, 2001, 16:54:40
 Job time: 8560 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 18, 2001, 13:43:40 ; Search time 6591.86 Seconds
(without alignments)
225.367 Million cell updates/sec

Title: US-09-143-828-1

Perfect score: 2905
Sequence: 1 cctctgaaggtctagaatc.....aaaaaaaaaaaaaaaaaaaa 2905

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

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82: gb_pat2:*
83: em_htg0:*
84: gb_htg24:*
85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2807.6	96.6	4448	52	HSJ9936 Homo sapi
3	2651.2	91.3	2802	10	AF084644 Homo sapi
4	2575.6	88.7	4337	52	HSJ9937 Homo sapi
5	2086.2	71.8	2146	10	AF061056 Homo sapi
6	1398.8	48.2	160185	69	AC069444 Homo sapi
7	1100.4	37.9	1885	3	AF182217 Oryctolagus
8	1006.8	34.7	1709	11	AF031814 Mus muscu
9	1004.2	34.6	1755	11	AF151377 Rattus no
10	991.4	34.1	1601	3	AF188476 Oryctolagus
11	335	11.5	365	77	G36929 SHGC-55597
12	284	9.8	1340	4	AF276753 Gallus ga
13	280.8	9.7	1377	11	MUSVDR
14	278.8	9.6	2043	11	RATDHYRDR3
15	275	9.5	2494	4	AF011356 Gallus ga
16	272.8	9.4	1284	10	AF026260 Homo sapi
17	272.8	9.4	1335	53	HSVD3R
18	272.8	9.4	4604	85	HUVD3R
19	267.8	9.2	1724	4	CJ012641 Coturnix ja
20	258.6	8.9	1638	4	XLRNANST
21	239.8	8.3	2429	4	AB037674 Paratrich

22	236.6	8.1	1503	4	AF1645512
23	236	8.1	1071	81	EL14584
24	232	8.0	1782	4	X1091846
25	230.4	7.9	2659	4	AB037673
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27	172.2	5.9	1450	53	HS00978
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29	170.6	5.9	1450	82	I73479
30	170.6	5.9	1450	82	EL1188
31	168.6	5.8	1350	11	AF009327
32	158.2	5.3	1077	11	AF133094
33	152.6	5.3	1077	11	AF133095
34	117.4	4.0	1332	11	AF009328
35	110.8	3.8	160185	69	AC069444
36	100.8	3.5	2797	32	DMU56792
37	100.8	3.5	113474	58	AC013932
38	100.8	3.5	116280	54	AC007853
39	100.8	3.5	161891	54	AC008206
40	100.8	3.5	227398	30	AE003750
41	100.4	3.5	1893	85	HUMVDRPMC
42	97.6	3.4	1208	81	I46765
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44	97.6	3.4	1979	81	AR035536
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RESULT 1	AF084645	2905 bp	mrna	PRI	20-OCT-1998
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DEFINITION	Homo sapiens orphan nuclear receptor (PAR1) mRNA, complete cds.				
ACCESSION	AF084645				
VERSION	AF084645.1	GI:3769358			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 2905) Berlilsson,G., Heidrich,J., Svensson,K., Asman,M., Jendeberg,L., Sydow-Backman,M., Ohlsson,R., Postlind,H., Blomquist,P. and Berkenstam,A.				
TITLE	Identification of a human nuclear receptor defines a new signalling pathway for CYP3A induction				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12208-12213 (1998)				
REFERENCE	2 (bases 1 to 2905) Berlilsson,G., Asman,M., Blomquist,P. and Berkenstam,A. •				
AUTHORS	Direct Submission				
TITLE	Submitted (19-AUG-1998) Cell and Molecular Biology, Medical Nobel Institute, Karolinska Institute, Doktorsringen2, Stockholm 17177, Sweden				
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[illegible]

AUTHORS Heard D.J., Holloway, J., Hansen, C., Tommerup, N., Aagaard, L. and Vissing, H.

TITLE Identification of a novel protein isoform of the human nuclear hormone receptor PXR/SXR and localization to chromosome 3q12.1-13.3

JOURNAL Eur. J. Hum. Genet. In press

REFERENCE 2 (bases 1 to 4448)

AUTHORS Heard, D.J.

TITLE Direct Submission

JOURNAL Submitted (31-JUL-1998) Heard D.J., Novo Nordisk A/S, Molecular Genetics, Novo Alle, DK-2880, Bagsvaerd, DENMARK

FEATURES

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CDS

BASE COUNT 1157 a 1132 c 1095 g 1064 t

ORIGIN

Query Match 96.6%; Score 2807.6; DB 52; Length 4448;
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2802)
 AUTHORS Bertilsson, G., Heideich, J., Svensson, K., Asman, M., Jendberg, L.,
 Sydow-Bachman, M., Ohlsson, R., Postlind, H., Blomquist, P. and
 Berkenstam, A.
 TITLE Identification of a human nuclear receptor defines a new signaling
 pathway for CYP3A induction
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12208-12213 (1998)
 MEDLINE 98445350
 REFERENCE 2 (bases 1 to 2802)

AUTHORS Bertilsson, G., Asman, M., Blomquist, P. and Berkenström, A.
 TITLE Direct Submission
 JOURNAL Submitted (19-AUG-1998) Cell and Molecular Biology, Medical Nobel
 Institute, Karolinska Institute, Doktorsringen 2, Stockholm 17177,
 Sweden

FEATURES

source

Location/Qualifiers

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ATTN	Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE	1 (pages 1 to 4337)
JOURNAL	Heard, D.J., Holloway, J., Hansen, C., Tommerup, N., Aagaard, L. and
REFERENCE	Vissing, H.
ATTN	Identification of a novel protein isoform of the human nuclear
TITLE	hormone receptor PXR/SXR and localization to chromosome 3q12.1
JOURNAL	133
REFERENCE	Eur. J. Hum. Genet. In press
ATTN	2 (pages 1 to 4337)
TITLE	Heard, D.J.
JOURNAL	Direct Submisson
REFERENCE	Submitted (31-JUL-1998) Heard D.J., Novo Nordisk A/S, Molecular
ATTN	Genetics, Novo Alle, DK-2880, Bagsvaerd, DENMARK
TITLE	Location/Qualifiers
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DEFINITION	Oryctolagus cuniculus pregnane x receptor (NR112) mRNA, complete cds.				
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VERSION	AF182217.1	GI:5853353			
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ORGANISM					
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REFERENCE	1 (bases 1 to 1895) Savas,U., Wester,M.R., Griffin,K.J. and Johnson,E.F. Rabbit pregnane X receptor is activated by rifampicin Drug Metab. Dispos. 28 (3), 529-537 (2000)				
AUTHORS					
TITLE					
JOURNAL					
MEDLINE	2 (bases 1 to 1895) Savas,U., Wester,M.R., Griffin,K.J. and Johnson,E.F. Direct Submission Submitted (01-SEP-1999) Division of Biochemistry, The Scripps Research Institute, 10550 North Torrey Pines Rd., La Jolla, CA 92037				
FEATURES	location/Qualifiers				
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QY	236	caaaagaacttaccaccaagcagtcgaagaagcccaagaagcaaaactggaagtgaagccca	295
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 Rattus.

REFERENCE 1 (bases 1 to 1755)
 AUTHORS Zhang, H., Leculysse, E., Liu, L., Hu, M., Matoney, L., Zhu, W. and Yan, B.
 TITLE Rat Pregnane X Receptor: Molecular Cloning, Tissue Distribution, and Xenobiotic Regulation
 JOURNAL Archive of Biochemistry and Biophysics 368 (1), 14-22 (1999)
 PUBMED 10415106

REFERENCE 2 (bases 1 to 1755)
 AUTHORS Zhang, H., Leculysse, E., Liu, L., Hu, M., Matoney, L., Zhu, W. and Yan, B.
 TITLE Direct Submission
 JOURNAL Submitted (13-MAY-1999) Biomedical Sciences, University of Rhode Island, 41 Lower College Road, Kingston, RI 02881, USA
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 source location/Qualifiers

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DEFINITION Oryctolagus cuniculus pregnancy X receptor (PXR) mRNA, complete cds
ACCESSION AF188476
VERSION AF188476.1
KEYWORDS GI:6901679
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 1601)
AUTHORS Jones,S.A., Moore,L.B., Shenk,J.L., Wisely,G.B., Hamilton,G.A.,
McKee,D.D., Tomkinson,N.C., LeCluyse,E.L., Lambert,M.H.,
Willson,T.M., Kilewer,S.A. and Moore,J.T.
The pregnane X receptor: a promiscuous xenobiotic receptor that has
diverged during evolution
Mol. Endocrinol. 14 (1), 27-39 (2000)
JOURNAL 20092326
MEDLINE 10628245
PUBMED 2
REFERENCE 2 (bases 1 to 1601)
AUTHORS Jones,S.A., Moore,L.B., Shenk,J.L., Wisely,G.B., Hamilton,G.A.,
McKee,D.D., Tomkinson,N.C., LeCluyse,E.L., Lambert,M.H.,
Willson,T.M., Kilewer,S.A. and Moore,J.T.
Direct Submission
Submitted (20-SEP-1999) Molecular Endocrinology, Glaxo Wellcome, 5
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REFERENCE	1 (bases 1 to 365)
AUTHORS	Myers,R.M.
TITLE	Human STS (1997)
JOURNAL	Unpublished (1997)
COMMENT	

Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myerseshgc.stanford.edu
Primer A: CCCATCAAGTGGCAAAACAGA
Primer B: AGTCAGAGTTCGACAGACA
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Denaturation: 94 degrees C for 30 seconds

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ORGANISM	Gallus gallus

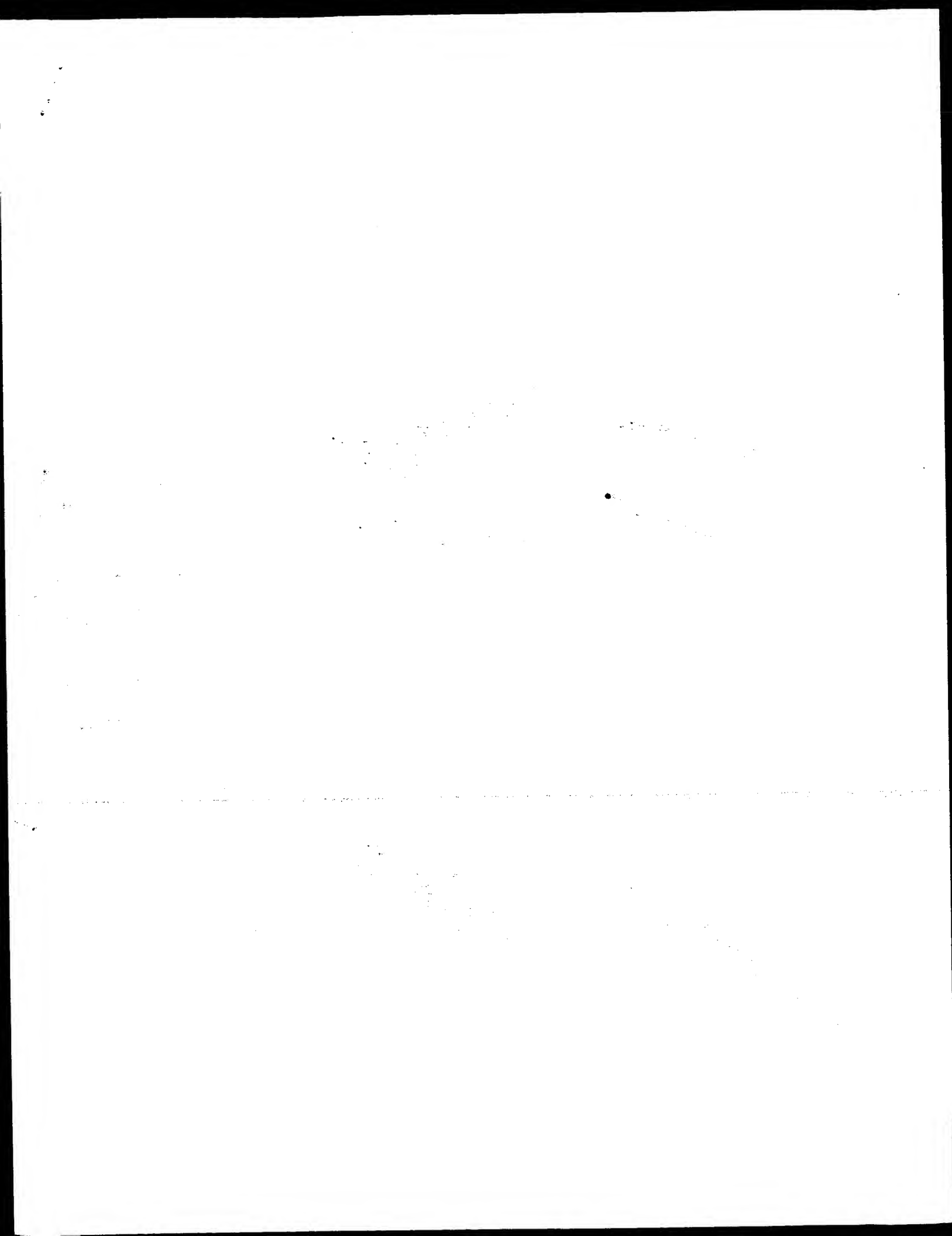
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QY 1 MEVPRKSNHADVHCEDTESPGKPSVNADEVEGPOICRVCGDKATGYHFNWTCGG 60
 DB 40 LEVPRKSNHADVHCEDTESPGKPSVNADEVEGPOICRVCGDKATGYHFNWTCGG 99
 QY 61 CKGFPRAMRNARLRCPPFKGACETTRKTRRQCCARLRCLESQMKKEMIMSDAAYE 120
 DB 100 CKGFPRAMRNARLRCPPFKGACETTRKTRRQCCARLRCLESQMKKEMIMSDAAYE 159
 QY 121 RRALIKRKKSERTGTPGLVQGLTEBQRMIRLMDAQKTEDTTFSHKNFRLPGVLS 180
 DB 160 RRALIKRKKSERTGTPGLVQGLTEBQRMIRLMDAQKTEDTTFSHKNFRLPGVLS 219
 QY 181 GCELPESLOAPSRBEAKMSQVARKDLSKVSQQLRGEDGSVWNNKPPADSGKEIFSL 240
 DB 220 GCELPESLOAPSRBEAKMSQVARKDLSKVSQQLRGEDGSVWNNKPPADSGKEIFSL 279
 QY 241 PHMADSTYMKGIISFAKVISYFRDLPTEDQISLKGAFELCOLRNTVFNATGTWE 300
 DB 280 PHMADSTYMKGIISFAKVISYFRDLPTEDQISLKGAFELCOLRNTVFNATGTWE 339
 QY 301 CGRLSTCLEDYAGGFOQLLEPMKFKHYMLKQLHHEEYVLMQALISLSPDRPGVLOHR 360
 DB 340 CGRLSTCLEDYAGGFOQLLEPMKFKHYMLKQLHHEEYVLMQALISLSPDRPGVLOHR 399
 QY 361 VVDQLOEOPAFITLKYIECNRPQAPARFLFKIMAMTELRSINQHTORLLRIODIHF 420
 DB 400 VVDQLOEOPAFITLKYIECNRPQAPARFLFKIMAMTELRSINQHTORLLRIODIHF 459
 QY 421 ATPMOELFGITGS 434
 DB 460 ATPMOELFGITGS 473

RESULT 2

Q9UJ27 PRELIMINARY: PRT: 434 AA.
 AC Q9UJ27;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-OCT-2000 (TREMblrel. 13, Last annotation update)
 DE NUCLEAR HORMONE RECEPTOR PRRI-A.
 GN PRRI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard L.,
 RA Vissing H.;
 RT "Identification of a novel protein isoform of the human nuclear
 RT hormone receptor PKR and localization to chromosome 3q12.1
 RT -13.3.";
 RL Eur. J. Hum. Genet. 9:0-0(0).
 DR EMBL: AJ009936; CAB55489.1
 DR HSSP: P10826; 1HRA.
 DR INTERPRO: IPR000324;
 DR INTERPRO: IPR000536;
 DR INTERPRO: IPR001628;
 DR INTERPRO: IPR001723;
 DR PFAM: PF00104; hormone_rec. 1.
 DR PFAM: PF00105; zf-C4. 1.
 DR PRINTS: PR00047; STROIDFINGER.
 DR PRINTS: PR00350; VITAMINDR.
 DR PRINTS: PR00398; STRDHOMONER.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR. 1.
 KW Receptor.
 SQ SEQUENCE 434 AA: 49777 MW: 4836DECC3C4C4200 CRC64;

Query Match

99.6%, Score 2281, DB 4; Length 434;

Best Local Similarity 99.5%; Pred. No. 2e-184;
Matches 432; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEVPRKSNHADVHCEDTESPGKPSVNADEVEGPOICRVCGDKATGYHFNWTCGG 60
 DB 1 MEVPRKSNHADVHCEDTESPGKPSVNADEVEGPOICRVCGDKATGYHFNWTCGG 60
 QY 61 CKGFPRAMRNARLRCPPFKGACETTRKTRRQCCARLRCLESQMKKEMIMSDAAYE 120
 DB 61 CKGFPRAMRNARLRCPPFKGACETTRKTRRQCCARLRCLESQMKKEMIMSDAAYE 120
 QY 121 RRALIKRKKSERTGTPGLVQGLTEBQRMIRLMDAQKTEDTTFSHKNFRLPGVLS 180
 DB 121 RRALIKRKKSERTGTPGLVQGLTEBQRMIRLMDAQKTEDTTFSHKNFRLPGVLS 180
 QY 181 GCELPESLOAPSRBEAKMSQVARKDLSKVSQQLRGEDGSVWNNKPPADSGKEIFSL 240
 DB 181 GCELPESLOAPSRBEAKMSQVARKDLSKVSQQLRGEDGSVWNNKPPADSGKEIFSL 240
 QY 241 PHMADSTYMKGIISFAKVISYFRDLPTEDQISLKGAFELCOLRNTVFNATGTWE 300
 DB 241 PHMADSTYMKGIISFAKVISYFRDLPTEDQISLKGAFELCOLRNTVFNATGTWE 300
 QY 301 CGRLSTCLEDYAGGFOQLLEPMKFKHYMLKQLHHEEYVLMQALISLSPDRPGVLOHR 360
 DB 301 CGRLSTCLEDYAGGFOQLLEPMKFKHYMLKQLHHEEYVLMQALISLSPDRPGVLOHR 360
 QY 361 VVDQLOEOPAFITLKYIECNRPQAPARFLFKIMAMTELRSINQHTORLLRIODIHF 420
 DB 361 VVDQLOEOPAFITLKYIECNRPQAPARFLFKIMAMTELRSINQHTORLLRIODIHF 420
 QY 421 ATPMOELFGITGS 434
 DB 421 ATPMOELFGITGS 434

RESULT 3

Q9UJ26 PRELIMINARY: PRT: 457 AA.
 AC Q9UJ26;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE NUCLEAR HORMONE RECEPTOR PRRI-C.
 GN PRRI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard L.,
 RA Vissing H.;
 RT "Identification of a novel protein isoform of the human nuclear
 RT hormone receptor PKR and localization to chromosome 3q12.1
 RT -13.3.";
 RL Eur. J. Hum. Genet. 9:0-0(0).
 DR EMBL: AJ009936; CAB55490.1
 DR HSSP: P10826; 1HRA.
 DR INTERPRO: IPR000324;
 DR INTERPRO: IPR000536;
 DR INTERPRO: IPR001628;
 DR INTERPRO: IPR001723;
 DR PFAM: PF00104; hormone_rec. 1.
 DR PFAM: PF00105; zf-C4. 1.
 DR PRINTS: PR00047; STROIDFINGER.
 DR PRINTS: PR00350; VITAMINDR.
 DR PRINTS: PR00398; STRDHOMONER.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR. 1.
 KW Receptor.
 SQ SEQUENCE 457 AA: 52145 MW: 812FB8B354B5B784E CRC64;

Query Match 99.5%; Score 2276; DB 4; Length 457;
 Best Local Similarity 99.3%; Pred. No. 3.8e-184;
 Matches 431; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB 1 MEVPRKESNNADPVHCDTESVPGKPSVNADEYGGPOICRVCGDKATGHHFNMTCGG 60
 DB 24 LEVPRKESNNADPVHCDTESVPGKPSVNADEYGGPOICRVCGDKATGHHFNMTCGG 83
 QY 61 CKGFERRAKNNARLRCFRRKACETITRTKROCOACRLKRCLESCKMKEMIMSDAEVEE 120
 DB 84 CKGFERRAKNNARLRCFRRKACETITRTKROCOACRLKRCLESCKMKEMIMSDAEVEE 143
 QY 121 RRALKRKRSRTGTQPLGVGGLTEEQRMIMRELMDAQMTFTDTSFHFNRPLGVLS 180
 DB 144 RRALKRKRSRTGTQPLGVGGLTEEQRMIMRELMDAQMTFTDTSFHFNRPLGVLS 203
 QY 181 RRALKRKRSRTGTQPLGVGGLTEEQRMIMRELMDAQMTFTDTSFHFNRPLGVLS 240
 DB 204 GCELPESLQAPSRREAAKNSQVRKDCSLKYSLOLRGSDGSWMYKPPADSGGKEIFSL 263
 QY 241 PHMADSTYMEKGIISPAKVISYFRDPIEDQISLKGAEELCOLRNTVFNAETGWE 300
 DB 264 PHMADSTYMEKGIISPAKVISYFRDPIEDQISLKGAEELCOLRNTVFNAETGWE 323
 QY 301 CGRLSTCLEDTAGGFOQLLEPMLKFFHYMLKTLQHEEYVLMQATSLFSPDRGVLOHR 360
 DB 324 CGRLSTCLEDTAGGFOQLLEPMLKFFHYMLKTLQHEEYVLMQATSLFSPDRGVLOHR 383
 QY 361 VVDLOEOFAITLKSYTECNRPQPAHRELFKIMAMTELRSINAQHTORLLRIQDIHPF 420
 DB 384 VVDLOEOFAITLKSYTECNRPQPAHRELFKIMAMTELRSINAQHTORLLRIQDIHPF 443
 QY 421 ATPLMQELFGITGS 434
 DB 444 ATPLMQELFGITGS 457

RESULT 4
 ID 090J24 PRELIMINARY; PRT; 397 AA.

AC 090J24; PRELIMINARY; PRT; 397 AA.
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
 DE NUCLEAR HORMONE RECEPTOR PRR2-A.
 GN PRR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard L.,
 RA Vissing H.;
 RT *Identification of a novel protein isoform of the human nuclear
 RT hormone receptor PKR/SXK and localization to chromosome 3q12.1
 RT -13.3.*;
 RL Eur. J. Hum. Genet. 0:0-0(0)
 DR EMBL: AJ009937; CAB5492.1;
 DR HSSP: P10826; IHRA.
 DR INTERPRO: IPR000324;
 DR INTERPRO: IPR000536;
 DR INTERPRO: IPR001628;
 DR INTERPRO: IPR001723;
 DR INTERPRO: IPR001728;
 DR PFAM: PF00104; hormone_rec; 1.
 DR PFAM: PF00105; zf-C4; 1.
 DR PRINTS: PR00047; STEROIDINGER.
 DR PRINTS: PR00350; VITAMINR.
 DR PRINTS: PR00398; STRDHOMONR.
 DR PRINTS: PR00546; THYROIDHOMR.

DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 KW Receptor.
 SQ SEQUENCE 397 AA; 45782 MW; 5E2CE0BB10663073 CRC64;

Query Match 90.0%; Score 2061.5; DB 4; Length 397;
 Best Local Similarity 91.0%; Pred. No. 5.8e-166;
 Matches 395; Conservative 0; Mismatches 2; Indels 37; Gaps 1;

QY 1 MEVPRKESNNADPVHCDTESVPGKPSVNADEYGGPOICRVCGDKATGHHFNMTCGG 60
 DB 1 MEVPRKESNNADPVHCDTESVPGKPSVNADEYGGPOICRVCGDKATGHHFNMTCGG 60
 QY 61 CKGFERRAKNNARLRCFRRKACETITRTKROCOACRLKRCLESCKMKEMIMSDAEVEE 120
 DB 61 CKGFERRAKNNARLRCFRRKACETITRTKROCOACRLKRCLESCKMKEMIMSDAEVEE 120
 QY 121 RRALKRKRSRTGTQPLGVGGLTEEQRMIMRELMDAQMTFTDTSFHFNRPLGVLS 180
 DB 121 RRALKRKRSRTGTQPLGVGGLTEEQRMIMRELMDAQMTFTDTSFHFNRPLGVLS 180
 QY 181 RRALKRKRSRTGTQPLGVGGLTEEQRMIMRELMDAQMTFTDTSFHFNRPLGVLS 240
 DB 181 RRALKRKRSRTGTQPLGVGGLTEEQRMIMRELMDAQMTFTDTSFHFNRPLGVLS 240
 QY 241 PHMADSTYMEKGIISPAKVISYFRDPIEDQISLKGAEELCOLRNTVFNAETGWE 300
 DB 241 PHMADSTYMEKGIISPAKVISYFRDPIEDQISLKGAEELCOLRNTVFNAETGWE 300
 QY 301 CGRLSTCLEDTAGGFOQLLEPMLKFFHYMLKTLQHEEYVLMQATSLFSPDRGVLOHR 360
 DB 301 CGRLSTCLEDTAGGFOQLLEPMLKFFHYMLKTLQHEEYVLMQATSLFSPDRGVLOHR 360
 QY 361 VVDLOEOFAITLKSYTECNRPQPAHRELFKIMAMTELRSINAQHTORLLRIQDIHPF 420
 DB 361 VVDLOEOFAITLKSYTECNRPQPAHRELFKIMAMTELRSINAQHTORLLRIQDIHPF 420
 QY 421 ATPLMQELFGITGS 434
 DB 421 ATPLMQELFGITGS 434
 QY 444 ATPLMQELFGITGS 457
 DB 444 ATPLMQELFGITGS 457

RESULT 5
 ID 090J23 PRELIMINARY; PRT; 420 AA.

AC 090J23; PRELIMINARY; PRT; 420 AA.
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
 DE NUCLEAR HORMONE RECEPTOR PRR2-C.
 GN PRR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard L.,
 RA Vissing H.;
 RT *Identification of a novel protein isoform of the human nuclear
 RT hormone receptor PKR/SXK and localization to chromosome 3q12.1
 RT -13.3.*;
 RL Eur. J. Hum. Genet. 0:0-0(0)
 DR EMBL: AJ009937; CAB5493.1;
 DR HSSP: P10826; IHRA.
 DR INTERPRO: IPR000324;
 DR INTERPRO: IPR000536;
 DR INTERPRO: IPR001628;
 DR INTERPRO: IPR001723;
 DR INTERPRO: IPR001728;
 DR PFAM: PF00104; hormone_rec; 1.
 DR PFAM: PF00105; zf-C4; 1.

DR PRINTS: PR00047; STROIDFINGER.
 DR PRINTS: PR00350; VITAMINDR.
 DR PRINTS: PR00398; STRDHOMONER.
 DR PRINTS: PR00546; THYROIDHOMER.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 DR RECEPTOR.
 KW RECEPTOR.
 SQ SEQUENCE 420 AA; 48149 MW; CFAD9EL256859165 CRC64;

Query Match 89.9%; Score 2058.5; DB 4; Length 420;
 Best Local Similarity 90.8%; Pred. No. 1.1e-165;
 Matches 394; Conservative 1; Mismatches 2; Indels 37; Gaps 1;

QY 1 MEVPRKSNHADVCEDETSVPGKPSVNADEVGPGQICRYCGDKATGIFPNVTCGG 60
 :|||||
 DB 24 LEVRPESNHNHDFVHCEDESVPGKPSVNADEVGPGQICRYCGDKATGIFPNVTCGG 83
 :|||||
 QY 61 CKGFFRRKRNARLRCPPRKACETTRKTRQCCACRLKCLSGMKKEMMSDEAVAE 120
 :|||||
 DB 84 CKGFFRRKRNARLRCPPRKACETTRKTRQCCACRLKCLSGMKKEMMSDEAVAE 143
 :|||||
 QY 121 RRALIRKKKSERTGTPGLVGGLTEQRMIRLMDAOMKTFDTTSHKFNRLP 180
 :|||||
 DB 144 RRALIRKKKSERTGTPGLVGGLTEQRMIRLMDAOMKTFDTTSHKFNRLP 196
 :|||||
 QY 181 GCELPESLQAPSRERAKMSQVRKDCSLKVSQLRGEGSVWYKPPADSGGKEIFSL 240
 :|||||
 DB 197 -----VSLQLRGEGSVWYKPPADSGGKEIFSL 226
 :|||||
 QY 241 PHNADSTYMEKGIISFAKVISYFRLPIEDQISLKGAFELCOLRFNTVFAETGWE 300
 :|||||
 DB 227 PHNADSTYMEKGIISFAKVISYFRLPIEDQISLKGAFELCOLRFNTVFAETGWE 286
 :|||||
 QY 301 CGRLSTYLEDYAGFQOLLLEPMKLFHYMLKTIQHEEYVLMQAIISLSPDRPGVLOHR 360
 :|||||
 DB 287 CGRLSTYLEDYAGFQOLLLEPMKLFHYMLKTIQHEEYVLMQAIISLSPDRPGVLOHR 346
 :|||||
 QY 361 VVDLOLOQOPATLKSTYECNRPOPAHREFLKIMAMTELRSINAOHTQRLRIQ 420
 :|||||
 DB 347 VVDLOLOQOPATLKSTYECNRPOPAHREFLKIMAMTELRSINAOHTQRLRIQ 406
 :|||||
 QY 421 ATPLMQELFGITGS 434
 :|||||
 DB 407 ATPLMQELFGITGS 420

RESULT 6
 ID 09UJ25 PRELIMINARY; PRT; 379 AA.
 AC 09UJ25;
 DT 01-MAY-2000 (Tribble, 13, Created)
 DT 01-MAY-2000 (Tribble, 13, Last sequence update)
 DT 01-OCT-2000 (Tribble, 15, Last annotation update)
 DE NUCLEAR HORMONE RECEPTOR PRL-B.
 GN PRL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RP TISSUE-LAYER;
 RC Heard D.J., Holloway J., Hansen C., Tommerup N., Aagaard L.,
 RA Vissing H.,
 RT "Identification of a novel protein isoform of the human nuclear
 RT hormone receptor PKR/SKR and localization to chromosome 3q12.1
 RT -13.3."
 RL Eur. J. Hum. Genet. 0:0-0(0).
 DR EMBL: AJ009936; CAB55491.1;
 DR HSSP: P10826; IHRA
 DR INTERPRO: IPR000324;
 DR INTERPRO: IPR000336;
 DR INTERPRO: IPR001628;

DR INTERPRO: IPR001723;
 DR PRAM: PR00104; hormone_rec; 1.
 DR PRAM: PR00105; zf-C4; 1.
 DR PRINTS: PR00047; STROIDFINGER.
 DR PRINTS: PR00350; VITAMINDR.
 DR PRINTS: PR00398; STRDHOMONER.
 DR PRINTS: PR00546; THYROIDHOMER.
 KW RECEPTOR.
 SQ SEQUENCE 379 AA; 43692 MW; 8F7B7AFAL3E45036 CRC64;

Query Match 86.2%; Score 1973; DB 4; Length 379;
 Best Local Similarity 99.7%; Pred. No. 1.6e-158;
 Matches 378; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 56 MTCGCKGFFRRKRNARLRCPPRKACETTRKTRQCCACRLKCLSGMKKEMMSD 115
 :|||||
 DB 1 MTCGCKGFFRRKRNARLRCPPRKACETTRKTRQCCACRLKCLSGMKKEMMSD 60
 :|||||
 QY 116 EAVEERRALIRKKKSERTGTPGLVGGLTEQRMIRLMDAOMKTFDTTSHKFNRLP 175
 :|||||
 DB 61 EAVEERRALIRKKKSERTGTPGLVGGLTEQRMIRLMDAOMKTFDTTSHKFNRLP 120
 :|||||
 QY 176 GYLSGCGELPESLQAPSRERAKMSQVRKDCSLKVSQLRGEGSVWYKPPADSGGKE 235
 :|||||
 DB 121 GYLSGCGELPESLQAPSRERAKMSQVRKDCSLKVSQLRGEGSVWYKPPADSGGKE 180
 :|||||
 QY 236 IFSLLPHNADSTYMEKGIISFAKVISYFRLPIEDQISLKGAFELCOLRFNTVFAE 295
 :|||||
 DB 181 IFSLLPHNADSTYMEKGIISFAKVISYFRLPIEDQISLKGAFELCOLRFNTVFAE 240
 :|||||
 QY 296 TGTWECGRSLSTYLEDYAGFQOLLLEPMKLFHYMLKTIQHEEYVLMQAIISLSPDRPG 355
 :|||||
 DB 241 TGTWECGRSLSTYLEDYAGFQOLLLEPMKLFHYMLKTIQHEEYVLMQAIISLSPDRPG 300
 :|||||
 QY 356 VLOHNVVDLOLOQOPATLKSTYECNRPOPAHREFLKIMAMTELRSINAOHTQRLRIQ 415
 :|||||
 DB 301 VLOHNVVDLOLOQOPATLKSTYECNRPOPAHREFLKIMAMTELRSINAOHTQRLRIQ 360
 :|||||
 QY 416 DIHPATPLMQELFGITGS 434
 :|||||
 DB 361 DIHPATPLMQELFGITGS 379

RESULT 7
 ID 09TU02 PRELIMINARY; PRT; 411 AA.
 AC 09TU02;
 DT 01-MAY-2000 (Tribble, 13, Created)
 DT 01-MAY-2000 (Tribble, 13, Last sequence update)
 DT 01-OCT-2000 (Tribble, 15, Last annotation update)
 DE PREGNANE X RECEPTOR.
 GN NR112 OR PKR.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 OX NCBI_TaxID=9986;
 RP SEQUENCE FROM N.A.
 RP STRAIN-BRED NEW ZEALAND WHITE RABBIT; TISSUE-KIDNEY;
 RC SAVES U., WESTER M.R., GRIFFIN K.J., JOHNSON E.F.;
 RA "The rabbit pregnane x receptor is activated by rifampicin."
 RT Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:20092326; PubMed:10628745;
 RA Jones S.A., Moore L.B., Shenk J.L., Wisely G.B., Hamilton G.A.,
 RA McKee D.D., Tomkinson N.C., Lecluyse E.L., Lambert M.H., Willison T.M.,
 RA Klierer S.A., Moore J.T.;
 RT "The pregnane X-receptor: a promiscuous xenobiotic receptor that has
 RT diverged during evolution."
 RL MOL. Endocrinol. 14:27-39(2000).
 DR EMBL: AF182217; RAD54426.1;
 DR EMBL: AF188476; AAF31165.1;

DR INTERPRO: IPRO01628; -
 DR INTERPRO: IPRO01723; -
 DR INTERPRO: IPRO01728; -
 DR PRAM: PF00104; hormone_rec; 1.
 DR PRAM: PF00105; zt-C4; 1.
 DR PRINTS: PRO0047; STROIDFINGER.
 DR PRINTS: PRO0350; VITAMINDR.
 DR PRINTS: PRO0398; STRODHOMNER.
 DR PRINTS: PRO0546; THYROIDHORM.
 DR RECEPTOR.
 DR SEQUENCE 342 AA; 3696 MW; 709467C3E9000A3A CRC64;

Query Match 76.6%; Score 1753.5; DB 4; Length 342;
 Best Local Similarity 90.0%; Pred. No. 4.7e-140;
 Matches 341; Conservative 0; Mismatches 1; Indels 37; Gaps 1;

QY 56 MTCGCKGFFRRAMKRNALRCPPKACETTRTRRQCACRLKCLSGMKKEMIMSD 115
 DB 1 MTCGCKGFFRRAMKRNALRCPPKACETTRTRRQCACRLKCLSGMKKEMIMSD 60
 QY 116 EAVERRALLIRKKSERGTGTPGVGITEEQRMMIRELMDAOKTDTTTFSHKFRLP 175
 DB 61 EAVERRALLIRKKSERGTGTPGVGITEEQRMMIRELMDAOKTDTTTFSHKFR-- 118
 QY 176 GVLSSGCELPESLQAPSHREAAKMSOVRKDLCSLKSLSLQSGEDGSVMNKKPPADSGKE 235
 DB 119 -----VSLQLRGEGGSVMNKKPPADSGKE 143
 QY 236 IFSLLPHNADSTYMGKGISFAVYSYFNDLPEDDISLKGAFELCOLRNTVYNAE 295
 DB 144 IFSLLPHNADSTYMGKGISFAVYSYFNDLPEDDISLKGAFELCOLRNTVYNAE 203
 QY 296 TGTGECGRSLCYLDDTAGGQQQLLEPMKFNHYLTKLQHEEYVYMOAISLSPDRPG 355
 DB 204 TGTGECGRSLCYLDDTAGGQQQLLEPMKFNHYLTKLQHEEYVYMOAISLSPDRPG 263
 QY 356 VLOHRVVDQLOEOPAITLKSTIECNRPQAPARFLFLKIMAMTELRSINAQHTQLRLIQ 415
 DB 264 VLOHRVVDQLOEOPAITLKSTIECNRPQAPARFLFLKIMAMTELRSINAQHTQLRLIQ 323
 QY 416 DIHPFATPIMOELFGITGS 434
 DB 324 DIHPFATPIMOELFGITGS 342

RESULT 10
 Q91839 PRELIMINARY; PRT; 386 AA.
 ID Q91839;
 AC Q91839;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DE 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE ORPHAN NUCLEAR RECEPTOR OF STEROID/THYROID SUPERFAMILY.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCB1_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94173664; PubMed=8127656;
 RA Smith D.P., Mason C.S., Jones E.A., Old R.W.;
 RT "A novel nuclear receptor superfamily member in Xenopus that
 RT associates with RXR, and shares extensive sequence similarity to the
 RT mammalian vitamin D3 receptor."
 RL Nucleic Acids Res. 22:66-71(1994).
 DR EMBL: X75163; CAA53006.1; -
 DR HSSP: P10826; IHRA.
 DR INTERPRO: IPRO00536; -
 DR INTERPRO: IPRO01628; -
 DR PRAM: PF00104; hormone_rec; 1.
 DR PRAM: PF00105; zt-C4; 1.

DR PRINTS: PRO0047; STROIDFINGER.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; UNKNOWN.1.
 DR SEQUENCE 386 AA; 44302 MW; 88046ED219556573 CRC64;

Query Match 43.3%; Score 991.5; DB 13; Length 386;
 Best Local Similarity 49.0%; Pred. No. 1.1e-75;
 Matches 204; Conservative 59; Mismatches 104; Indels 49; Gaps 9;

QY 18 EDTESVPGKPSVNADEYGGPOICVCGDKATGYHFNMTCEGCKGFFRRAMKRNALRC 77
 DB 14 EDEEASNSGCTGEDEDDGDPKICRACDPRATGYHFNMTCEGCKGFFRRAMKRNALRC 73
 QY 78 PPRKACETTRTRRQCACRLKCLSGMKKEMIMSEAVERRALLIRK-KSERGTQ 136
 DB 74 PF-QNSCVINKSNRHCQACRLKCLDYGKRELIMSDAAVQRALIRKHKLTLPPT 132
 QY 137 PLVGGLTEEQMMIRELMDAOKTDTTTFSHKFRLPGLVSSGCELPESLQAPSHREA 196
 DB 133 PPGA-SLPEEQHFLQLVGATKTFDENFTFSKFR-----PIR--- 171
 QY 197 AFWSOVRKDL:SLKVSLSLQSGEDGSVMNKKPPADSGKEITSLPHNADSTYMGKGIS 256
 DB 172 -----RSSDPT--QEPQATS--SEATLMPHISDLTYIMKIGIS 207
 QY 257 FAKVISYFNDLPEDDISLKGAFELCOLRNTVYNAEFGTTCGRLCYCLDPT-AGGF 315
 DB 208 FAKMLPTFSLSLQGLDIALKGSVAEYVIRNVTFSNDITWEGGPTTYTEMFLAGF 267
 QY 316 QQLLEPMKFNHYLTKLQHEEYVYMOAISLSPDRPGVLOHRVVDQLOEOPAITLKS 375
 DB 268 RQLFLEPLVIRHMRKNTLQSEEVYAMMAALSTASDRPGVCDMEKIKQLQEHATLTKD 327
 QY 376 YIECNR-PPQAPARFLFLKIMAMTELRSINAQHTQLRIODIHPFATPIMOELFG 430
 DB 328 FIDSQRPSPQRLLYPRIMCLETETLVNDIHSKQLLEIMDIODATPLMRVEVG 383

RESULT 11
 Q91B73 PRELIMINARY; PRT; 420 AA.
 ID Q91B73;
 AC Q91B73;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE VITAMIN D RECEPTOR A.
 GN VDRA.
 OS Paratichthys olivaceus (Flounder).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
 OC Pleuronectidae; Boichidae; Paratichthys.
 NC NCB1_TaxID=8253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RA Suzuki T., Suzuki N., Sriwastava A.S., Kurokawa T.;
 RT "Identification of cDNAs encoding two subtypes of vitamin D receptor
 RT in flounder, Paratichthys olivaceus."
 RL Biochem. Biophys. Res. Commun. 270:40-45(2000).
 DR EMBL: AB037674; BAA95016.1; -
 DR RECEPTOR.
 DR SEQUENCE 420 AA; 47486 MW; 038FBF00D4F38067 CRC64;

Query Match 35.7%; Score 817; DB 13; Length 420;
 Best Local Similarity 43.1%; Pred. No. 6.3e-61;
 Matches 179; Conservative 70; Mismatches 144; Indels 22; Gaps 12;

QY 29 VNADG-ETGGPOICRVCGDKATGYHFNMTCEGCKGFFRRAMKRNALRCPPKACETIT 87
 DB 11 VGPDEFRRNARICGVCQDKATGFHFNAMTCEGCKGFFRRAMKRNALRCPPKACETIT 69


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OY 88 KTRRQCCACRLKCLSGMKKEMIMSDAVERBALIKRKSEGTGTPIGVGLTEEQ 147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 70 KNRHRCQACRLKRCIDIGMKKEFILTDEVOGREKEMILKREEDANEARPR-LNEQ 128
OY 148 RMIRIELMDAOKTPTDTFSHKRNLRLP---GVLSGCELPESLOABREDAKMSOYRK 204
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 ARMISLVEAHKRTYDASDSFRPRPVRECPVTRASRAASLSHSDASDSFNHSE 188
OY 205 DLCSLV---SLQNGEDSVYNNYKPPADSGKEIFSLPHADSTWNGTISFANVI 261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 SV-DIKMFSNLMYQOGA-----SSPSSEENTKLSMLPHADLVSTIOKIVGFAKI 243
OY 262 SYFRDLPIEDQISLKGAFELCOLRFTVNAETGTECG--RLSTCYLED-TAGGFQOL 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 PGRDLTAEEDQIALKSSAIEITIMLRNSQSFLEDMSCGCPPEKVCINDVTKAGHLE 303
OY 319 LLEPLKTHYMLKTLQLEHEEVYLMQALSLSPDRPGTLQIRVYDQLOEQALTKSTIE 378
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 304 LLEPLKTHYMLKTLQLEHEEVYLMQALSLSPDRPGTLQIRVYDQLOEQALTKSTIE 378
OY 379 CNRPQPAHRLFLKIMAMLTSLRSINAQHTO--RLLRIDIHFP-ATPLMOELFG 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 364 IN--HGGRLLYAKMIQKLDLRLSINEHRSKQYSLSTQSPHSMQUTPLVLEVFG 416

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RESULT 12

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O9PTN2 09PTN2 PRELIMINARY: PRT: 453 AA.
AC O9PTN2:
DT 01-MAY-2000 (TREMELREL. 13, Created)
DT 01-MAY-2000 (TREMELREL. 13, Last sequence update)
DT 01-OCT-2000 (TREMELREL. 15, Last annotation update)
DE VITAMIN D RECEPTOR.
GN VDR.
OS Brechydario reio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7953;
RN [1]
RP SEQUENCE FROM N.A.
RA Kouzmenko A.P.;
RT "Danio reio vitamin D receptor.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF164512; AAF21427.1;
DR HSSP; P20393; 1A6Y.
DR INTERPRO; IPR000534;
DR INTERPRO; IPR000536;
DR INTERPRO; IPR001628;
DR INTERPRO; IPR001723;
DR PFM; PF00104; hormone_rec; 1.
DR PFM; PF00105; zf-C4; 1.
DR PRINTS; PRO0047; STROIDFINGER.
DR PRINTS; PRO0350; VITAMINDR.
DR PRINTS; PRO0398; STRIDROMER.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor.
SQ SEQUENCE 453 AA; 50765 MW; B52C82C185859F9C CRC64;

```

Query Match 34.6%; Score 792; DB 13; Length 453;
 Best Local Similarity 40.3%; Pred. No. 8.9e-59;
 Matches 178; Conservative 74; Mismatches 158; Indels 32; Gaps 11;

```

OY 7 ESNHADFVCEDETVGKPSVNADEVEGPOICRVCGDKATGYHFNWTCGCGGPR 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 22 ESTYNGDASTLMDLAVSTISATGODPDNRAPICVCGDKATGYHFNWTCGCGGPR 81
OY 67 RAKRNRALCPRKAGCEITRTTRQCCACRLKCLSGMKKEMIMSDAVERBALIK 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 82 RSMKRKASFTCPF-NGNCTITKDNRRHRCQACRLKRCIDIGMKKEFILTDEVOGRKDDLM 140
OY 127 RKSE---RTGTQPIAGVGLTEQGRMIRIELMDAOKTPTDTFSHKRNLRLP---GVLS 180

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Db 141 KRKEEAKARAP-----RLSDROMQINSLVAHKKTYDDSDVRFRPPVRECPVTR 196
OY 181 GCELPESLOAPREDAKMS-----QVRDLCSLVSQNGEDSVYNNYKPPADSGK 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 SASRAASLSHSDASSDSFNHSPESVDTLNTNSLNMQODSGSPS-----SEDOQ 249
OY 235 EITSLPHADNMITYFKGISPAKVISYFRDLPIEDQISLKGAFELCOLRFTVNA 294
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 250 SRLSMLPHADLVSTIOKIVGFAKIPGRDLTAEEDQIALKSSAIEITIMLRNSQSF 309
OY 295 ETGTWECG--RLSTCYLED-TAGGFQOLLEPLKTHYMLKTLQLEHEEVYLMQALSLSP 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 310 EDMNSGCGEPFYKCYINDVTKAGHTELEPLKTHYMLKTLQLEHEEVYLMQALSLSP 369
OY 352 DRPGVLOHRYVQLOQAFATIKSYTECNRPQPAHRLFLKIMAMLTSLRSINAQHTO-- 409
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 370 DRPGVLOHRYVQLOQAFATIKSYTECNRPQPAHRLFLKIMAMLTSLRSINAQHTO-- 409
OY 410 RLLRIDIHF-ATPLMOELFG 430
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 428 RSLSTQSPHSMQUTPLVLEVFG 449

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RESULT 13

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O9IB74 09IB74 PRELIMINARY: PRT: 425 AA.
AC O9IB74:
DT 01-OCT-2000 (TREMELREL. 15, Created)
DT 01-OCT-2000 (TREMELREL. 15, Last sequence update)
DT 01-OCT-2000 (TREMELREL. 15, Last annotation update)
DE VITAMIN D RECEPTOR B.
GN VDRB.
OS Parichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorph; Pleuronectiformes;
OC Pleuronectidae; Boichidae; Parichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-INTESTINE;
RA Suzuki T., Suzuki N., Srivastava A.S., Kurokawa T.;
RT Identification of cDNAs encoding two subtypes of vitamin D receptor
  in flounder, Parichthys olivaceus.
RL Biochem. Biophys. Res. Commun. 270:40-45(2000).
DR EMBL; AB037673; BAA95015.1;
KW Receptor.
SQ SEQUENCE 425 AA; 48174 MW; 7B1D49CF4C2C65E9 CRC64;

```

Query Match 34.5%; Score 790.5; DB 13; Length 425;
 Best Local Similarity 41.6%; Pred. No. 1.1e-58;
 Matches 179; Conservative 78; Mismatches 140; Indels 33; Gaps 13;

```

OY 22 SVPGKPSVNADE-VEVGPOICRVCGDKATGYHFNWTCGCGGPRAMKRNALRCPFR 80
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4 TVYSSSLASDEFDNMRRICVCGDKATGYHFNWTCGCGGPRAMKRNALRCPFR 62
OY 81 KGACEITRTTRQCCACRLKCLSGMKKEMIMSDAVERBALIKRK-----SRT 133
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 NSCSITKDNRRHRCQACRLKRCIDIGMKKEFILTDEVOGRKDDLMQKDEAREARE 122
OY 134 GTPGVLGVLTEQGRMIRIELMDAOKTPTDTFSHKRNLRLP---GVLSGCELPESLOA 190
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 AARP-----RLTDEQSOVYAMVEAHKRTYDSDYDFCFRPPVRECPVTRASRAASLS 178
OY 191 PSREDAKMSQVRKDLCSLVS-----LQNGEDSVYNNYKPPADSGKEIFSLPHADM 246
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 LSDASSDSFSHPESV-DTKYFNKMLMYOEGS-----SPDSSEEGSSFSMLPHADL 233
OY 247 STYKKGISPAKVISYFRDLPIEDQISLKGAFELCOLRFTVNAETGTWECGR--L 304
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 234 VSXIOKVIQFAMIPGFELETAEDQIALKSSALEVIMLRNSQNFENEDMSWCGADPF 293
OY 305 SYCLEL-TAGGPOQLLEPMKPFHYMLKKILOHEEYVMOAISLSPDRPGVLOHRVD 363
Db 294 KIOISDVYTAGHTLELEPLVYKFOVGLKLNLOEEHVMALICLSPRPVQOHARIE 353
OY 364 QLOEOPATLKSYTECNRPDPAHFLFKIMAMTELRSINAOHTO--RLNRIDIHFP- 420
Db 354 ALDDBRISETLOAVIOLH--HPGRLLYAKMIQKIALDRSLRINEHRSKQYSLSFREHSMQ 411
OY 421 ATPLOELEG 430
Db 412 LTPVLEVSG 421

RESULT 14
OY00U1 PRELIMINARY; PRT; 358 AA.
AC OY00U1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE NUCLEAR RECEPTOR.
GN CAR.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR KYOTO, AND FISCHER;
RA Yoshinari K., Sueyoshi T., Moore R., Negishi M.;
RT "Sexually dimorphic nuclear translocation of receptor CAR and
RT induction of CYP2B1 gene by phenobarbital in rat livers."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ133095; AAF22567.1; -
DR EMBL: AF133094; AAF22566.1; -
DR HSSP: P13793; 2ML.
DR INTERPRO: IPR000324; -
DR INTERPRO: IPR000536; -
DR INTERPRO: IPR001628; -
DR INTERPRO: IPR001723; -
DR INTERPRO: IPR001728; -
DR PFAM: PF00104; hormone_rec. 1.
DR PFAM: PF00105; zf-C4; 1.
DR PRINTS: PR00047; STROIDFINGER.
DR PRINTS: PR00350; VITAMINDR.
DR PRINTS: PR00398; STRDHOMONER.
DR PRINTS: PR00546; THYROIDHORMR.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor.
SQ SEQUENCE 358 AA; 40922 MW; 13691F49CAD8F1ED CRC64;

Query Match 31.8%; Score 729; DB 11; Length 358;
Best Local Similarity 40.3%; Pred. No. 1.4e-53;
Matches 160; Conservative 61; Mismatches 122; Indels 54; Gaps 6;
OY 33 EEVGGPOICRVCGDKATGYHFNVMTCEGCGFFRRAMKRNARLCPFRKGCETTRKTR 92
Db 13 EEYGPFRVCVCGDRATGYHFHALTEGCGFFRRVSKTIGPICPF-AGCEVCQAOR 71
OY 93 OCOACRLKCLSGMKKIMINSDEAVERBALIKRKSEPTGTOLPVGOTEEORAMIR 152
Db 72 HCPACRLKCLVNGKRMKMLISAEPLALRRARRRRAOKASLO-----LSQOKELIQ 125
OY 153 ELMDAQMTFTTFSHFNFRLPGVLSGCELPESIOAPSBEEAKMSQVRRKDISLKV 212
Db 126 TLGGHTRHVGPMFQYQFRRPAYLFSH-HRPFQPLAP----- 163
OY 213 IOLREDSQWNYKPPADSGGKEITSLLPHADMTYFKGLISPAKIVISFROLPIEDQ 272
Db 164 -----VPLLTHTFADINTFWVOQIIKFTKOLPLFRSLTMDQ 200

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OY 273 ISLKGAPELCQURENTVNAETGMEGCRSLSYCLEDTAG-GEQOULLPEMLKPFHYMLK 331
Db 201 ISLKGAPELITISLTTFCLOTFONFCPLCYKEDAVHGFQFELELIHFHFKITLK 260
OY 332 KLOHEEYVMOAISLSPDRPGVLOHRVDOLOEOPATLKSYTECNRPDPAHFLFL 391
Db 261 RLOEPEPYALMAMALFSPDRPGVLOHREIIDLQEEVALIINNHIMEQSRLOSRFLVA 320
OY 392 KIMAMTELRSINAOHTORLIRIDIHFPATPLMOEL 428
Db 321 KIMGLAEIRLSINAGSYEIRIOLGSLAM-MPLIGEI 356

RESULT 15
OY00U7 PRELIMINARY; PRT; 445 AA.
AC OY00U7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE NUCLEAR OXYSTEROL RECEPTOR LXR-ALPHA (LXR-ALPHA).
GN NR1H3 OR LXR-ALPHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVJ; TISSUE=LIVER;
RA Albert S., Steffensen K.R., Gustafsson J.A.;
RT "Cloning and characterisation of nuclear oxysterol receptor genes LXRA
RT and LXRb from mouse."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ132599; CAB51952.1; -
DR EMBL: AJ132601; CAB51952.1; JOINED.
DR HSSP: P20393; 1A6Y.
DR MGD: MGI:1352462; Nr1h3.
DR INTERPRO: IPR000324; -
DR INTERPRO: IPR000536; -
DR INTERPRO: IPR000923; -
DR INTERPRO: IPR001628; -
DR INTERPRO: IPR001723; -
DR INTERPRO: IPR001728; -
DR INTERPRO: IPR003069; -
DR INTERPRO: IPR003078; -
DR PFAM: PF00104; hormone_rec. 1.
DR PFAM: PF00105; zf-C4; 1.
DR PRINTS: PR00047; STROIDFINGER.
DR PRINTS: PR00350; VITAMINDR.
DR PRINTS: PR00398; STRDHOMONER.
DR PRINTS: PR00546; THYROIDHORMR.
DR PRINTS: PR01283; ECDYSTEROIDR.
DR PRINTS: PR01282; RETINOICACIDR.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
DR PROSITE: PS00196; COPPER_BLUE; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 445 AA; 50476 MW; CC9ABDF38D935593 CRC64;

Query Match 22.0%; Score 504.5; DB 11; Length 445;
Best Local Similarity 30.4%; Pred. No. 1.6e-34;
Matches 130; Conservative 85; Mismatches 142; Indels 71; Gaps 13;
OY 18 EDETSPPKPSVNADEVEGPOICRVCGDKATGYHFNVMTCEGCGFFRRAMKRNARLRC 77
Db 73 EPTLPQKRRKPPAKMLGNELCSYCGKASGFHTNYLSGCGGFFRRSVYIKARVYC 132
OY 78 PFRKGA CETTRKTRQOACRLKCLSGMKKIMINSDEAVERRALIKRKSE----- 131
Db 133 -HSGGHPDVTYRRKRCQCRKRCQACMRRECVLSQIRLKR--LKROEEQOATS 189

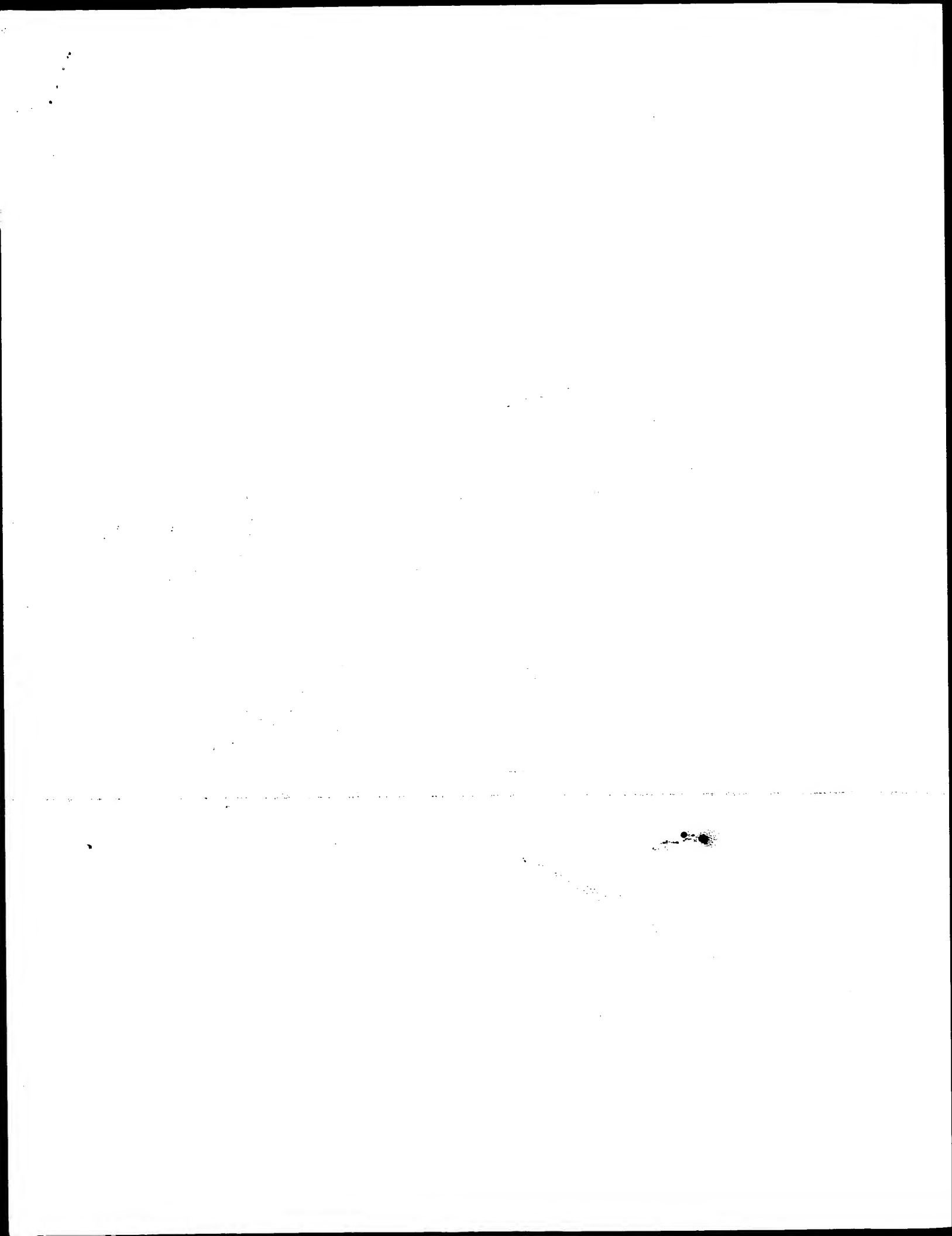
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QY 132 ---RTGTPGLGVGLTEQRMRELMDAQKTFDTTSHFNKRLPGVLSGCELPESL 188
Db 190 VSPRVSSPPQVLPQLSPQLEMIKELVAAOQCNRBSFS----- 228
QY 189 QAPSRFEAAKWSQVRKDCSLKVSJLGRGEDGSVWNYKPPADSGKREIFSLPHMADMT 248
Db 229 ---DRLATPR-PIAPD-----POSREARQORFA--HTELA 260
QY 249 YMEGIIISFAKVISYFRLPIEDQISLKGAFELCOLRENTVEN--AETGTECGRLSY 306
Db 261 VSVQEIYDFAKQLPGFIQLSREDOIALKTSALIEVMLETSSRYNPGSESITF-LKDFGY 319
QY 307 CLEPTA-GGFQOLLLEPMLKFHYMLKQLHEBEYVLMQALISLSPDRPGVLOHRYVDOL 365
Db 320 NREDFAKAGQVEFINPIEFESRAMMELQINDAEFALLIAISIFSADRPVQCLOVERL 379
QY 366 QEOFAITLKSIECNRPQAPAHREFLEFKIMAMTELRSINAOHTORL--LRIDIHFPATP 423
Db 380 QHTYVEALHAYVSINHPH--DRLMFPMLKLVSLRTLSVHSEQYFALRLD--KLLPP 435
QY 424 LMQELFGI 431
Db 436 LLSIEMDV 443

```

Search completed: February 18, 2001, 13:05:04
 Job time: 6193 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 18, 2001, 12:12:43 ; Search time 63.99 Seconds

(without alignments)
231.913 Million cell updates/sec

Title: US-09-143-828-2

Perfect score: 2290

Sequence: 1 MEYRPRESNMHADVHCEDT.....ODIHPRATPLMQELFCITGS 434

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: /cgn2_2/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /cgn2_2/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /cgn2_2/gcgdata/geneseq/geneseq/AA1982.DAT.*
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21: /cgn2_2/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2290	100.0	437	20	Y09515 Human vitamin D re
2	2287	98.9	434	20	Y15931 A human intranucle
3	2287	98.9	457	20	Y16035 A human intranucle
4	2287	99.9	457	20	Y15932 A human intranucle
5	2287	99.9	466	20	Y25410 Human NMR7 partial
6	2287	99.9	473	20	Y25411 Human NMR7-1 prote
7	2287	99.9	473	20	Y15936 A human intranucle
8	2287	99.9	473	20	Y15933 A human intranucle
9	2287	99.9	473	20	Y09516 Human vitamin D re
10	2169	94.7	434	20	Y21799 Human steroid and
11	2165	94.5	414	20	Y42691 Human pregnane X r
12	1585	69.2	316	20	Y42689 Hsb-pregnane X re

13	979.5	42.8	386	17	R98521
14	801	35.0	423	20	W45623
15	798	34.8	423	19	W47509
16	789	34.5	427	19	W68156
17	789	34.5	427	20	Y09064
18	789	34.5	450	20	Y09036
19	789	34.5	477	20	Y09035
20	768	33.5	348	18	W32536
21	768	33.5	348	20	W39002
22	763	33.3	348	14	R41346
23	733.5	32.0	357	20	Y17872
24	725	31.7	358	20	W33903
25	656	28.6	356	19	W37261
26	656	28.6	356	20	W45622
27	632	27.6	367	14	R43656
28	498.5	21.8	445	21	Y32374
29	498	21.7	460	16	R74738
30	498	21.7	461	15	R32980
31	498	21.7	461	17	R37982
32	498	21.7	461	17	R38140
33	496	21.7	460	18	W25034
34	495	21.6	461	17	R66234
35	491.5	21.5	447	17	W03326
36	490	21.4	446	17	R39736
37	487	21.3	446	17	R94169
38	483	21.1	443	16	R74739
39	483	21.1	443	18	W25035
40	481.5	21.0	440	14	R33744
41	469.5	20.5	472	19	W40072
42	454	19.8	469	17	W03448
43	451.5	19.7	484	17	R39735
44	448	19.6	456	9	P80921
45	445	19.4	461	20	Y21631

ALIGNMENTS

RESULT	1
ID	Y09515
Y09515	standard; Protein: 437 AA.
XX	
AC	Y09515:
XX	
DT	16-JUL-1999 (first entry)
XX	
DE	Human vitamin D receptor related gamma protein.
XX	
KW	Human: vitamin D receptor related protein; VDR; obesity; diabetes; anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia; hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; tumour; hyperproliferative skin disorder; hyperthyroidism.
KW	Homo sapiens.
OS	
PN	W09919354-A1.
XX	
PD	22-APR-1999.
XX	
PF	31-AUG-1998: 98WO-SE01548.
XX	
PR	31-MAR-1998: 98SE-0001148.
PR	14-OCT-1997: 97SE-0003745.
PA	(PHAA) PHARMACIA & UPJOHN AB.
XX	
PI	Berkenstam A, Dahlberg M;
XX	
DR	WPI: 1999-302508/25.
XX	
PT	N-FSDB; X56242.
XX	
PT	New vitamin D receptor related (VDR) polypeptides, useful for treating obesity, diabetes, anorexia and rheumatoid arthritis

Xenopus orphan rec
Rat vitamin D rece
Rat vitamin D rece
Human vitamin D re
Human vitamin D re
Human vitamin D re
Human vitamin D re
Constitutively act
Human CAR receptor
Human CAR receptor
Mouse nuclear rece
Mouse CAR receptor
Rat vitamin D rece
Rat vitamin D rece
Mouse CNREB-1. Mu
Human ubiquitinous n
Human recombinant
Human steroid rece
NER receptor poten
Human foetal lung
LXR-alpha, orphan
Retinoid X recepto
OR-1 orphan recept
Rat ubiquitinous nuc
XR2. Homo sapiens
Human retinoid rec
Retinoid X recepto
Sequence encoded b
Ligand binding dom

XX Claim 19; Page 19-20; 35pp; English.

CC The present sequence is a human vitamin D receptor related (VDR)
 CC polypeptide. Human VDR polypeptides and substances which affect VDR
 CC signal transduction, can be used for treating metabolic, proliferative
 CC or inflammatory conditions. They can be used in the manufacture of a
 CC medicament for treating the following conditions: obesity, diabetes,
 CC anorexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or
 CC hyperlipoproteinaemia and osteoporosis, rheumatoid arthritis, Dengign and
 CC malign tumours, hyperproliferative skin disorders or hyperthyroidism.
 CC Nucleic acid vectors encoding for expression of a VDR polypeptide can
 CC be used for treating metabolic, proliferative or inflammatory conditions,
 CC by introducing them into a mammal. The introduced nucleic acid is then
 CC capable of transforming a cell in vitro and then polypeptide is expressed.
 CC A substance affecting VDR signal transduction, such as an agonist or
 CC antagonist can be used for the manufacture of a medicament for treating
 CC metabolic, proliferative or inflammatory condition.
 CC N.B. The specification specifically claims the VDR nucleic acid and
 CC polypeptide sequences given in figures 1, 4, 7 and 8, but no figures
 CC are given in the specification.

XX Sequence 437 AA;

Query Match 100.0%; Score 2290; DB 20; Length 437;
 Best Local Similarity 100.0%; Pred. No. 7.7e-219;
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVPRKESWNHADFVCEDESVPGRPSVNADEVGPGQICRYCGDKATGYHFNWTCG 60
 DB 1 MEVPRKESWNHADFVCEDESVPGRPSVNADEVGPGQICRYCGDKATGYHFNWTCG 60
 QY 61 CCGFRRRAKRNARLRCPPRRKACETTRKTRQCCACRLRKLCSGKMKEMMSDEAYVE 120
 DB 61 CCGFRRRAKRNARLRCPPRRKACETTRKTRQCCACRLRKLCSGKMKEMMSDEAYVE 120
 QY 121 RRALIRKKKSERTGPTLGVQGLTEEOGRMIRELMDAOKTEPDTFSHKNFRLPGVLS 180
 DB 121 RRALIRKKKSERTGPTLGVQGLTEEOGRMIRELMDAOKTEPDTFSHKNFRLPGVLS 180
 QY 181 GCELPESLQAPSEBAKMSQVRKDCSLKVSLOLRGEGSVWYKPPADSGGKEIFSL 240
 DB 181 GCELPESLQAPSEBAKMSQVRKDCSLKVSLOLRGEGSVWYKPPADSGGKEIFSL 240
 QY 241 PHMAKSTYMFKGIISFAVVISYFRDLPREDQISLKGAAPFLCQRFNTVNAETGWE 300
 DB 241 PHMAKSTYMFKGIISFAVVISYFRDLPREDQISLKGAAPFLCQRFNTVNAETGWE 300
 QY 301 CGRLSYCLEDTAGGFOQLLEPMLKFHYMLKKQLHEEYVLMQATSLFSPDRPGVLOHR 360
 DB 301 CGRLSYCLEDTAGGFOQLLEPMLKFHYMLKKQLHEEYVLMQATSLFSPDRPGVLOHR 360
 QY 361 VVDQLOEFAITLKSYTECNRPQAPARFLFLKIMAMTELRSINAOHTQRLRIQDHPF 420
 DB 361 VVDQLOEFAITLKSYTECNRPQAPARFLFLKIMAMTELRSINAOHTQRLRIQDHPF 420
 QY 421 ATPLMQELFGITGS 434
 DB 421 ATPLMQELFGITGS 434

RESULT 2

Y15931 ID Y15931 standard; Protein; 434 AA.

Y15931; AC Y15931;

04-AUG-1999 (first entry)

A human intranuclear receptor protein.

Human; intranuclear receptor protein; drug development; diagnosis;

KW treatment.

OS Homo sapiens.

PN JP1127872-A.

PD 18-MAY-1999.

PF 07-AUG-1998; 98UP-0224172.

PR 11-AUG-1997; 97UP-0230335.

PA (NISH) JAPAN TOBACCO, INC.

DR WPI: 1999-350330/30.

DR N-PSDB; X59966.

PT New intranuclear receptor protein - useful for drug development and

PS diagnosis and treatment of disease

CC Claim 1; Page 15-16; 38pp; Japanese.

CC The present sequence represents a human intranuclear receptor protein.
 CC The nucleic acid sequence was isolated from a human adult cDNA
 CC library using a swillfish AMO23 derived probe. The protein can
 CC be used for the development of drugs and diagnosis and treatment
 CC of various diseases.

XX Sequence 434 AA;

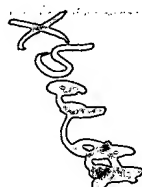
Query Match 99.9%; Score 2287; DB 20; Length 434;
 Best Local Similarity 99.8%; Pred. No. 1.5e-218;
 Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVPRKESWNHADFVCEDESVPGRPSVNADEVGPGQICRYCGDKATGYHFNWTCG 60
 DB 1 MEVPRKESWNHADFVCEDESVPGRPSVNADEVGPGQICRYCGDKATGYHFNWTCG 60
 QY 61 CCGFRRRAKRNARLRCPPRRKACETTRKTRQCCACRLRKLCSGKMKEMMSDEAYVE 120
 DB 61 CCGFRRRAKRNARLRCPPRRKACETTRKTRQCCACRLRKLCSGKMKEMMSDEAYVE 120
 QY 121 RRALIRKKKSERTGPTLGVQGLTEEOGRMIRELMDAOKTEPDTFSHKNFRLPGVLS 180
 DB 121 RRALIRKKKSERTGPTLGVQGLTEEOGRMIRELMDAOKTEPDTFSHKNFRLPGVLS 180
 QY 181 GCELPESLQAPSEBAKMSQVRKDCSLKVSLOLRGEGSVWYKPPADSGGKEIFSL 240
 DB 181 GCELPESLQAPSEBAKMSQVRKDCSLKVSLOLRGEGSVWYKPPADSGGKEIFSL 240
 QY 241 PHMAKSTYMFKGIISFAVVISYFRDLPREDQISLKGAAPFLCQRFNTVNAETGWE 300
 DB 241 PHMAKSTYMFKGIISFAVVISYFRDLPREDQISLKGAAPFLCQRFNTVNAETGWE 300
 QY 301 CGRLSYCLEDTAGGFOQLLEPMLKFHYMLKKQLHEEYVLMQATSLFSPDRPGVLOHR 360
 DB 301 CGRLSYCLEDTAGGFOQLLEPMLKFHYMLKKQLHEEYVLMQATSLFSPDRPGVLOHR 360
 QY 361 VVDQLOEFAITLKSYTECNRPQAPARFLFLKIMAMTELRSINAOHTQRLRIQDHPF 420
 DB 361 VVDQLOEFAITLKSYTECNRPQAPARFLFLKIMAMTELRSINAOHTQRLRIQDHPF 420
 QY 421 ATPLMQELFGITGS 434
 DB 421 ATPLMQELFGITGS 434

RESULT 3

Y16035 ID Y16035 standard; Protein; 457 AA.

Y16035; AC Y16035;



XX 04-AUG-1999 (first entry)
 XX A human intranuclear receptor protein.
 DE Human; intranuclear receptor protein; drug development; diagnosis;
 KW treatment.
 XX Homo sapiens.
 OS JP1127872-A.
 PN 18-MAY-1999.
 PD 07-AUG-1998; 98JP-0224172.
 XX 11-AUG-1997; 97JP-0230335.
 XX (NISB) JAPAN TOBACCO INC.
 PA WPI: 1999-350330/30.
 DR N-PSDB; X59975.
 XX
 XX New intranuclear receptor protein - useful for drug development and
 PT diagnosis and treatment of disease
 PS Disclosure: Page 35-37; 38pp; Japanese.
 XX
 CC The present sequence represents a human intranuclear receptor protein.
 CC The nucleic acid sequence was isolated from a human adult cDNA
 CC library using a swillfish ANO23 derived probe. The protein can
 CC be used for the development of drugs and diagnosis and treatment
 CC of various diseases.
 XX
 SQ Sequence 457 AA;

Query Match 99.9%; Score 2287; DB 20; Length 457;
 Best Local Similarity 99.8%; Pred. No. 1.6e-218;
 Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVPRKESNMHADFYHCEPTESVPGKPSVNADEVGPGQICRVCGDKATGYHFNWTCG 60
 DB 24 LEVRKESNMHADFYHCEPTESVPGKPSVNADEVGPGQICRVCGDKATGYHFNWTCG 83
 QY 61 CKGFRRAMKRNARLRCPPRKACETTRKTRQCCACRLKCLSGMKEMKMSDAVEE 120
 DB 84 CKGFRRAMKRNARLRCPPRKACETTRKTRQCCACRLKCLSGMKEMKMSDAVEE 143
 QY 121 RRALKRKRSERTGTOPLGVOGLTEORMMIRELMDAOKTPTDTSHPKRNPLPGVLS 180
 DB 144 RRALKRKRSERTGTOPLGVOGLTEORMMIRELMDAOKTPTDTSHPKRNPLPGVLS 203
 QY 181 GCELPESIQAPSRERAKMSQVRKDCSLKVSQLRGEGSVWNYKPPADSGKEIFSL 240
 DB 204 GCELPESIQAPSRERAKMSQVRKDCSLKVSQLRGEGSVWNYKPPADSGKEIFSL 263
 QY 241 PHMADSTYMFKGIISFAKVISYFRDLPEDQISLKGAAPFELCOLRNTVPAETGWE 300
 DB 264 PHMADSTYMFKGIISFAKVISYFRDLPEDQISLKGAAPFELCOLRNTVPAETGWE 323
 QY 301 CGRLSYCTEDTAGGFOQLLEPMLKFHYMLKRLQHEEYVLMQATSLSPDRPGVLOHR 360
 DB 324 CGRLSYCTEDTAGGFOQLLEPMLKFHYMLKRLQHEEYVLMQATSLSPDRPGVLOHR 383
 QY 361 VVDOLQOPAITLKSYTECNRPOPARHFLFLKIMAMLTSLRSINAOHTORLLRIODIHP 420
 DB 384 VVDQIQEGFELTLKEYLEENRPGPAHFRFLKIMAMLTSLRSINAOHTORLLRIODIHP 443
 QY 421 ARPLMOELFGITGS 434
 DB 444 ARPLMOELFGITGS 457

RESULT 4
 ID Y15932
 Y15932 standard; Protein: 457 AA.
 AC Y15932;
 XX
 XX 04-AUG-1999 (first entry)
 DE A human intranuclear receptor protein.
 KW Human; intranuclear receptor protein; drug development; diagnosis;
 KW treatment.
 XX Homo sapiens.
 OS JP1127872-A.
 PN 18-MAY-1999.
 PD 07-AUG-1998; 98JP-0224172.
 XX 11-AUG-1997; 97JP-0230335.
 XX (NISB) JAPAN TOBACCO INC.
 PA WPI: 1999-350330/30.
 DR N-PSDB; X59967.
 XX
 XX New intranuclear receptor protein - useful for drug development and
 PT diagnosis and treatment of disease
 PS Claim 2; Page 16-17; 38pp; Japanese.
 XX
 CC The present sequence represents a human intranuclear receptor protein.
 CC The nucleic acid sequence was isolated from a human adult cDNA
 CC library using a swillfish ANO23 derived probe. The protein can
 CC be used for the development of drugs and diagnosis and treatment
 CC of various diseases.
 XX
 SQ Sequence 457 AA;

Query Match 99.9%; Score 2287; DB 20; Length 457;
 Best Local Similarity 99.8%; Pred. No. 1.6e-218;
 Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVPRKESNMHADFYHCEPTESVPGKPSVNADEVGPGQICRVCGDKATGYHFNWTCG 60
 DB 24 LEVRKESNMHADFYHCEPTESVPGKPSVNADEVGPGQICRVCGDKATGYHFNWTCG 83
 QY 61 CKGFRRAMKRNARLRCPPRKACETTRKTRQCCACRLKCLSGMKEMKMSDAVEE 120
 DB 84 CKGFRRAMKRNARLRCPPRKACETTRKTRQCCACRLKCLSGMKEMKMSDAVEE 143
 QY 121 RRALKRKRSERTGTOPLGVOGLTEORMMIRELMDAOKTPTDTSHPKRNPLPGVLS 180
 DB 144 RRALKRKRSERTGTOPLGVOGLTEORMMIRELMDAOKTPTDTSHPKRNPLPGVLS 203
 QY 181 GCELPESIQAPSRERAKMSQVRKDCSLKVSQLRGEGSVWNYKPPADSGKEIFSL 240
 DB 204 GCELPESIQAPSRERAKMSQVRKDCSLKVSQLRGEGSVWNYKPPADSGKEIFSL 263
 QY 241 PHMADSTYMFKGIISFAKVISYFRDLPEDQISLKGAAPFELCOLRNTVPAETGWE 300
 DB 264 PHMADSTYMFKGIISFAKVISYFRDLPEDQISLKGAAPFELCOLRNTVPAETGWE 323
 QY 301 CGRLSYCTEDTAGGFOQLLEPMLKFHYMLKRLQHEEYVLMQATSLSPDRPGVLOHR 360
 DB 324 CGRLSYCTEDTAGGFOQLLEPMLKFHYMLKRLQHEEYVLMQATSLSPDRPGVLOHR 383
 QY 361 VVDOLQOPAITLKSYTECNRPOPARHFLFLKIMAMLTSLRSINAOHTORLLRIODIHP 420

Db 384 vvdqieqfaatlksylecnpqphrflfkimamltelrsnaqhtqrlrlrldqdhpf 443
 Oy 421 ATPLMOELFGITGS 434
 Db 444 atplmgelfigtgs 457

RESULT 5
 Y25410
 ID Y25410 standard; Protein; 466 AA.

AC Y25410;
 DT 06-SEP-1999 (first entry)
 DE Human nNR7 partial protein.
 XX
 XX nNR7; nNR7-1; nuclear trans-acting receptor protein; human; regulator;
 KW identification; downstream target gene; cell proliferation;
 KM cell development.

XX Homo sapiens.
 OS
 XX MO9931129-A1.
 PN
 XX 24-JUN-1999.
 PD
 XX 11-DEC-1998; 98WO-US26364.
 PE
 XX 14-OCT-1998; 98US-0104251.
 PR 12-DEC-1997; 97US-0069401.
 XX
 XX (MERI) MERCK & CO INC.
 PA
 XX Chen F;
 PI
 XX WPI; 1999-405024/34.
 DR N-PSDB; X78807.
 DR
 XX

PT DNA encoding human nuclear receptors nNR7 and nNR7-1

PS Claim 1; Fig 3; 80pp; English.

CC This invention describes the isolation of the novel human nuclear
 CC receptors nNR7 or nNR7-1. The nNR7 and nNR7-1 proteins are useful in
 CC the identification of downstream target genes and ligands regulating its
 CC activity. The nuclear receptor is involved in the regulation of in vivo
 CC cell proliferation and/or cell development. The nNR7 and nNR7-1
 CC polynucleotides, expression vectors and host cells are useful for the
 CC recombinant production of the protein.

XX Sequence 466 AA;

Query Match 99.9%; Score 2287; DB 20; Length 466;
 Best Local Similarity 99.8%; Pred. No. 1.7e-218;
 Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MEVPRKESNNADFYHCEDTESVPEKPSVNADEYVGQICRVCGDKATGYHFNVMTCG 60
 Db 33 levprkeswnhadvfhcedtesvpgkpsvnadeevgpgqicrvcgdkatgyhfnvmctcg 92
 Oy 61 CKGFERRAMKRNARLRCPFRKACEITRKTRPROCAQRLRKRCESGKKKIMNSDEAVEE 120
 Db 93 ckgffrramkrnarlrpfrkaceitrtktrprocaqrlrkrcesgkkmimsdeavee 152
 Oy 121 RRALIKRKKSERGTQPLGVGLTEQRMIRLEMDAQMTFTTSHFNFRPLPGVLSS 180
 Db 153 rralikrkksergtqplgvglteqrmirlemdaqmtfttshfnfrplpyvlss 212
 Oy 181 GCELPESIQAPSRREAAKMSQVRKDCSLKYSQLRGEDSVWNYKRPADSGKEIFSL 240
 Db 213 gcelpesiqapsrreaaakmsqvrkdcslkysqlrgedsvwnykrpadsgkeifsl 272

Oy 241 PHMADSTYMEKGIISFAKVISYFRDLPIEDQISILKGAFAELCOLRNFVNAETGWE 300
 Db 273 phmadstymekgiisfakvisyfrdlpiedqisilksaafelcolrnfvnaetgwe 332
 Oy 301 CGRLSYCLEDFAGGFGQOLLLEPMLKFNHMKRIQDHEEYVLMQAIISFSPDRPGVLOHR 360
 Db 333 cgrlsycaledfagfgqolllepmlkfnhmkriqdhheeyvlmqaisfspdrgvlgohr 392
 Oy 361 VYDQLOEFPARTLKSTIECNRRQPARRFLFKIMAMLTFLRSINQHTORLLRQDHPF 420
 Db 393 vvdqieqfaatlksylecnpqphrflfkimamltelrsnaqhtqrlrlrldqdhpf 452
 Oy 421 ATPLMOELFGITGS 434
 Db 453 atplmgelfigtgs 466

RESULT 6
 Y25411
 ID Y25411 standard; Protein; 473 AA.

AC Y25411;
 DT 06-SEP-1999 (first entry)
 DE Human nNR7-1 protein.

XX nNR7; nNR7-1; nuclear trans-acting receptor protein; human; regulator;
 KW identification; downstream target gene; cell proliferation;
 KM cell development.

OS Homo sapiens.
 XX
 XX MO9931129-A1.
 PN
 XX 24-JUN-1999.
 PD
 XX 11-DEC-1998; 98WO-US26364.
 PE
 XX 14-OCT-1998; 98US-0104251.
 PR 12-DEC-1997; 97US-0069401.
 XX
 XX (MERI) MERCK & CO INC.
 PA
 XX Chen F;
 PI
 XX WPI; 1999-405024/34.
 DR N-PSDB; X78808.
 DR
 XX

PT DNA encoding human nuclear receptors nNR7 and nNR7-1

PS Claim 20; Fig 6; 80pp; English.

CC This invention describes the isolation of the novel human nuclear
 CC receptors nNR7 or nNR7-1. The nNR7 and nNR7-1 proteins are useful in
 CC the identification of downstream target genes and ligands regulating its
 CC activity. The nuclear receptor is involved in the regulation of in vivo
 CC cell proliferation and/or cell development. The nNR7 and nNR7-1
 CC polynucleotides, expression vectors and host cells are useful for the
 CC recombinant production of the protein.

XX Sequence 473 AA;

Query Match 99.9%; Score 2287; DB 20; Length 473;
 Best Local Similarity 99.8%; Pred. No. 1.7e-218;
 Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MEVPRKESNNADFYHCEDTESVPEKPSVNADEYVGQICRVCGDKATGYHFNVMTCG 60
 Db 40 levprkeswnhadvfhcedtesvpgkpsvnadeevgpgqicrvcgdkatgyhfnvmctcg 99

QY 61 CKGFFRRAMRNARLRCPPFRKGCETTRKTRQOCARLKLKESGKMKKEMSDAEVE 120
 DB 100 CCGFFRRAMRNARLRCPPFRKGCETTRKTRQOCARLKLKESGKMKKEMSDAEVE 159
 QY 121 RRALIRKRSKERTGTOTPLVQGLTEQRMVIRELMDAQKTFDTTSHKRNFLPGVLS 180
 DB 160 RRALIRKRSKERTGTOTPLVQGLTEQRMVIRELMDAQKTFDTTSHKRNFLPGVLS 219
 QY 181 GCELPESLQAPSRHEAKMSQVRKDCSLKVSQQLGEGDSVWVNYKPPADSGKEIFSL 240
 DB 220 GCELPESLQAPSRHEAKMSQVRKDCSLKVSQQLGEGDSVWVNYKPPADSGKEIFSL 279
 QY 241 PHADMSTYFKGISFAVVISYFRDLPEDQISLKGAFELCOLRFTVFAETGWE 300
 DB 280 PHADMSTYFKGISFAVVISYFRDLPEDQISLKGAFELCOLRFTVFAETGWE 339
 QY 301 CGRLSYCLSDTLAGFQQLLEPMLKHYMLKRLQLEHEEYVLMQALSLSPDRPGVLQHR 360
 DB 340 CGRLSYCLSDTLAGFQQLLEPMLKHYMLKRLQLEHEEYVLMQALSLSPDRPGVLQHR 399
 QY 361 VVDQLOEOPAITLKSYIECNRPQPAHRELFKIMAMTELRSINQHTORLRIODIHPF 420
 DB 400 VVDQLOEOPAITLKSYIECNRPQPAHRELFKIMAMTELRSINQHTORLRIODIHPF 459
 QY 421 ATPLMQELFGITGS 434
 DB 460 ATPLMQELFGITGS 473

RESULT 7

ID Y15936 standard; Protein; 473 AA.

XX Y15936;

DT 04-AUG-1999 (first entry)

DE A human intranuclear receptor protein.

KW Human; intranuclear receptor protein; drug development; diagnosis;

OS Homo sapiens.

PN JP1127872-A.

PD 18-MAY-1999.

PE 07-AUG-1998; 98JP-0224172.

PR 11-AUG-1997; 97JP-0230335.

PA (NISB) JAPAN TOBACCO INC.

DR WPI: 1999-350330/30.

DR N-PSDB; X59974.

PT New intranuclear receptor protein - useful for drug development and

PS diagnosis and treatment of disease

CC The present sequence represents a human intranuclear receptor protein.

CC The nucleic acid sequence was isolated from a human adult cDNA

CC library using a swedish ANO23 derived probe. The protein can

CC be used for the development of drugs and diagnosis and treatment

CC of various diseases.

SO Sequence 473 AA;

Query Match 99.9%; Score 2287; DB 20; Length 473;
 Best Local Similarity 99.8%; Pred. No. 1.7e-218;

Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEVPRKSNWHADEPVEDTESVGRKPVNADEVGPOICRVCGSKAGVHFNWTCG 60
 DB 40 IEVPRKSNWHADEPVEDTESVGRKPVNADEVGPOICRVCGSKAGVHFNWTCG 99
 QY 61 CKGFFRRAMRNARLRCPPFRKGCETTRKTRQOCARLKLKESGKMKKEMSDAEVE 120
 DB 100 CCGFFRRAMRNARLRCPPFRKGCETTRKTRQOCARLKLKESGKMKKEMSDAEVE 159
 QY 121 RRALIRKRSKERTGTOTPLVQGLTEQRMVIRELMDAQKTFDTTSHKRNFLPGVLS 180
 DB 160 RRALIRKRSKERTGTOTPLVQGLTEQRMVIRELMDAQKTFDTTSHKRNFLPGVLS 219
 QY 181 GCELPESLQAPSRHEAKMSQVRKDCSLKVSQQLGEGDSVWVNYKPPADSGKEIFSL 240
 DB 220 GCELPESLQAPSRHEAKMSQVRKDCSLKVSQQLGEGDSVWVNYKPPADSGKEIFSL 279
 QY 241 PHADMSTYFKGISFAVVISYFRDLPEDQISLKGAFELCOLRFTVFAETGWE 300
 DB 280 PHADMSTYFKGISFAVVISYFRDLPEDQISLKGAFELCOLRFTVFAETGWE 339
 QY 301 CGRLSYCLSDTLAGFQQLLEPMLKHYMLKRLQLEHEEYVLMQALSLSPDRPGVLQHR 360
 DB 340 CGRLSYCLSDTLAGFQQLLEPMLKHYMLKRLQLEHEEYVLMQALSLSPDRPGVLQHR 399
 QY 361 VVDQLOEOPAITLKSYIECNRPQPAHRELFKIMAMTELRSINQHTORLRIODIHPF 420
 DB 400 VVDQLOEOPAITLKSYIECNRPQPAHRELFKIMAMTELRSINQHTORLRIODIHPF 459
 QY 421 ATPLMQELFGITGS 434
 DB 460 ATPLMQELFGITGS 473

RESULT 8

ID Y15933 standard; Protein; 473 AA.

XX Y15933;

DT 04-AUG-1999 (first entry)

DE A human intranuclear receptor protein.

KW Human; intranuclear receptor protein; drug development; diagnosis;

OS Homo sapiens.

PN JP1127872-A.

PD 18-MAY-1999.

PE 07-AUG-1998; 98JP-0224172.

PR 11-AUG-1997; 97JP-0230335.

PA (NISB) JAPAN TOBACCO INC.

DR WPI: 1999-350330/30.

DR N-PSDB; X59968.

PT New intranuclear receptor protein - useful for drug development and

PS diagnosis and treatment of disease

CC The present sequence represents a human intranuclear receptor protein.

CC The nucleic acid sequence was isolated from a human adult cDNA

CC library using a swedish ANO23 derived probe. The protein can

CC be used for the development of drugs and diagnosis and treatment

CC of various diseases.

XX Sequence 473 AA;

Query Match 99.9%; Score 2287; DB 20; Length 473;
Best Local Similarity 99.8%; Pred. No. 1.7e-218;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVPRKESNMHADVHCEDTESVPGKPSVNADEVGPOICRVGDKATGYHFNVMTCES 60
:|||||
DB 40 LEVPRKESNMHADVHCEDTESVPGKPSVNADEVGPOICRVGDKATGYHFNVMTCES 99
QY 61 CKGFFRRAMRNARLCPFRKGCETIRKTRROCOACRLKCLSGMKKEMIMSDAEVE 120
:|||||
DB 100 CKGFFRRAMRNARLCPFRKGCETIRKTRROCOACRLKCLSGMKKEMIMSDAEVE 159
QY 121 RRALIRKKKSERTGTOPLGVOGLTEEQRMIRIEMDAOMKTFDTTSHFNKFLPGVLS 180
:|||||
DB 160 RRALIRKKKSERTGTOPLGVOGLTEEQRMIRIEMDAOMKTFDTTSHFNKFLPGVLS 219
QY 181 GCELPESLQAPSRREAAKWSQVRKDLCSLKVSIQLRGEDGSVMNKPAPDSGKEIFSL 240
:|||||
DB 220 GCELPESLQAPSRREAAKWSQVRKDLCSLKVSIQLRGEDGSVMNKPAPDSGKEIFSL 279
QY 241 PHMADMTVMFKGISFAKVISYFRDLPIEDQISLKGAFELCOLRNTVFNAETGWE 300
:|||||
DB 280 PHMADMTVMFKGISFAKVISYFRDLPIEDQISLKGAFELCOLRNTVFNAETGWE 339
QY 301 CGRLSTCLEDTAGFQOLLLEPMKLFHYMLKQLHBEERYVLMQASISFSDRPGVLOHR 360
:|||||
DB 340 CGRLSTCLEDTAGFQOLLLEPMKLFHYMLKQLHBEERYVLMQASISFSDRPGVLOHR 399
QY 361 VTDOLQEOFAITLKSYIECNRPQPAHRLFLKIMAMTELRISINAQHTQLRIODIHPE 420
:|||||
DB 400 VTDOLQEOFAITLKSYIECNRPQPAHRLFLKIMAMTELRISINAQHTQLRIODIHPE 459
QY 421 ATPLMOELFGITGS 434
:|||||
DB 460 ATPLMOELFGITGS 473

RESULT 9
ID Y09516 standard; Protein: 473 AA.
XX Y09516;
AC Y09516;
XX 16-JUL-1999 (first entry)
DE Human vitamin D receptor related gamma 2 protein.
XX
XX Human: vitamin D receptor related protein; VDR; obesity; diabetes;
KW anorexia; rheumatoid arthritis; lipoprotein defect; hyperlipidaemia;
KW hypercholesterolaemia; hyperlipoproteinaemia; osteoporosis; tumour;
KW hyperproliferative skin disorder; hyperthyroidism.
XX
OS Homo sapiens.
XX
XX W09919354-A1.
XX
XX 22-APR-1999.
XX
XX 31-AUG-1998; 98MO-SE01548.
XX
XX 31-MAR-1998; 98SE-0001148.
XX
XX 14-OCT-1997; 97SE-0003745.
XX
XX (PMAA) PHARMACIA & UPJOHN AB.
XX
XX Berkenstam A, Dahlberg M;
XX
XX WPI; 1999-302508/25.
XX
XX N-PSDB; X56243.

XX New vitamin D receptor related (VDR) polypeptides, useful for
PT treating obesity, diabetes, anorexia and rheumatoid arthritis
XX
XX Claim 19; Page 22-24; 35pp; English.

CC The present sequence is a human vitamin D receptor related (VDR)
CC polypeptide. Human VDR polypeptides and substances which affect VDR
CC signal transduction, can be used for treating metabolic, proliferative
CC or inflammatory conditions. They can be used in the manufacture of a
CC medicament for treating the following conditions: obesity, diabetes,
CC anorexia, lipoprotein defects, hyperlipidaemia, hypercholesterolaemia or
CC hyperlipoproteinaemia and osteoporosis, rheumatoid arthritis, benign and
CC malign tumours, hyperproliferative skin disorders or hyperthyroidism.
CC Nucleic acid vectors encoding for expression of a VDR polypeptide can
CC be used for treating metabolic, proliferative or inflammatory conditions,
CC by introducing them into a mammal. The introduced nucleic acid is then
CC capable of transforming a cell in vivo and then polypeptide is expressed.
CC A substance affecting VDR signal transduction, such as an agonist or
CC antagonist can be used for the manufacture of a medicament for treating
CC metabolic, proliferative or inflammatory condition.
CC N.B. The specification specifically claims the VDR nucleic acid and
CC polypeptide sequences given in figures 1, 4, 7 and 8, but no figures
CC are given in the specification.

SO Sequence 473 AA;

Query Match 99.9%; Score 2287; DB 20; Length 473;
Best Local Similarity 99.8%; Pred. No. 1.7e-218;
Matches 433; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEVPRKESNMHADVHCEDTESVPGKPSVNADEVGPOICRVGDKATGYHFNVMTCES 60
:|||||
DB 40 LEVPRKESNMHADVHCEDTESVPGKPSVNADEVGPOICRVGDKATGYHFNVMTCES 99
QY 61 CKGFFRRAMRNARLCPFRKGCETIRKTRROCOACRLKCLSGMKKEMIMSDAEVE 120
:|||||
DB 100 CKGFFRRAMRNARLCPFRKGCETIRKTRROCOACRLKCLSGMKKEMIMSDAEVE 159
QY 121 RRALIRKKKSERTGTOPLGVOGLTEEQRMIRIEMDAOMKTFDTTSHFNKFLPGVLS 180
:|||||
DB 160 RRALIRKKKSERTGTOPLGVOGLTEEQRMIRIEMDAOMKTFDTTSHFNKFLPGVLS 219
QY 181 GCELPESLQAPSRREAAKWSQVRKDLCSLKVSIQLRGEDGSVMNKPAPDSGKEIFSL 240
:|||||
DB 220 GCELPESLQAPSRREAAKWSQVRKDLCSLKVSIQLRGEDGSVMNKPAPDSGKEIFSL 279
QY 241 PHMADMTVMFKGISFAKVISYFRDLPIEDQISLKGAFELCOLRNTVFNAETGWE 300
:|||||
DB 280 PHMADMTVMFKGISFAKVISYFRDLPIEDQISLKGAFELCOLRNTVFNAETGWE 339
QY 301 CGRLSTCLEDTAGFQOLLLEPMKLFHYMLKQLHBEERYVLMQASISFSDRPGVLOHR 360
:|||||
DB 340 CGRLSTCLEDTAGFQOLLLEPMKLFHYMLKQLHBEERYVLMQASISFSDRPGVLOHR 399
QY 361 VTDOLQEOFAITLKSYIECNRPQPAHRLFLKIMAMTELRISINAQHTQLRIODIHPE 420
:|||||
DB 400 VTDOLQEOFAITLKSYIECNRPQPAHRLFLKIMAMTELRISINAQHTQLRIODIHPE 459
QY 421 ATPLMOELFGITGS 434
:|||||
DB 460 ATPLMOELFGITGS 473

RESULT 10
ID Y21799 standard; Protein: 434 AA.
XX Y21799;
AC Y21799;
XX
XX 14-SEP-1999 (first entry)
XX

DE Human steroid and xenobiotic receptor (SXR).
 XX
 KW Nuclear receptor; SXR; steroid and xenobiotic receptor; RXR; human;
 KW retinoid X receptor; P450 gene; steroid hormone; steroid metabolism;
 KW phytoestrogen; calcium-channel blocker; steroid toxicity; tuberculosis;
 KW breast cancer; osteoporosis; Cushing syndrome; virilism; hirsutism;
 KW polycystic ovarian disease; cancer; colorectal; prostatic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 227
 FT /label= unknown
 FT /note= "encoded by ACN"
 XX
 XX W09935246-A1.
 XX
 PD 15-JUL-1999.
 XX
 XX 08-JAN-1999; 99WO-US00490.
 XX
 XX 09-JAN-1998; 98US-0005286.
 XX
 XX (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 XX Blumberg B, Evans RM;
 XX
 XX WPI: 1999-410349/35.
 XX
 XX N-PSDB: X89080.
 XX
 XX
 PT New steroid and xenobiotic receptor, used to identify modulators for
 PT controlling metabolism of steroids and xenobiotics, e.g. reducing
 PT their toxicity
 PT
 PS Claim 4; Fig 1A; 83pp; English.
 PS
 XX
 XX The invention relates to a novel nuclear receptor polypeptide, designated
 CC SXR (steroid and xenobiotic receptor). SXR (1) forms a heterodimer with
 CC retinoid X receptor (RXR), (11) binds to a direct or inverted repeat
 CC response element motif based on the half-site AGTCA, (111) activates
 CC transcription through response elements present in steroid-inducible P450
 CC genes, in response to a wide variety of natural and synthetic steroid
 CC hormones and (1v) is prominently expressed in liver and intestine. SXR
 CC regulates expression of catabolic enzymes, in response to many different
 CC steroids, and thus affects metabolism. SXR is a broad specificity, low-
 CC affinity receptor for reducing excessive levels of steroids in the
 CC circulation. (Ant)agonists of SXR are used to regulate metabolism of
 CC steroids particularly phytoestrogens or calcium-channel blockers, to
 CC reduce steroid toxicity in subjects being treated with steroids, e.g. in
 CC cases of tuberculosis (treated with rifampin and related compounds),
 CC breast cancer (treated with tamoxifen, raloxifen etc.) or osteoporosis
 CC (treated with Vitamin K), or to slow metabolism of therapeutic steroids.
 CC Also, modulating endogenous SXR is used to treat disease, particularly
 CC an agonist is used where endogenous steroid levels are excessive (e.g.
 CC Cushing syndrome; virilism and hirsutism in women; polycystic ovarian
 CC disease; 11 beta-, 17- or 21-hydroxylase deficiency; 3 beta-hydroxysteroid
 CC dehydrogenase deficiency, or breast, colorectal or prostatic cancer),
 CC while antagonists are used where endogenous steroid levels are too low.
 CC Cells that express SXR are used to identify compounds likely to be
 CC involved in immunohistochemical testing for studying distribution/
 CC expression density of SXR, also for diagnosis and therapeutically as
 CC antagonist. The present sequence represents SXR polypeptide.
 CC
 XX
 SO Sequence 434 AA:

Query Match 94.7%; Score 2169; DB 20; Length 434;
 Best Local Similarity 95.6%; Pred No. 7.7e-207;
 Matches 415; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

1 MEVRPESNHNADPVHCDETSVPGKPSVNADEVGPOICRVCGDKATGYHFNMTCEG 60
 :|||||

DB 1 levyrkeswnhadvhcedteavpgrkpsvnaadevypqicrvcgdkatgyhfnmtceg 60
 OY 61 CKGEFFRAMRNRLCPFRKGACEITRKTROCCACRLKCESGKMKEMSDAEVBE 120
 DB 61 CKGFITRAMKRNRLCPFRKGACEITRKTROCCACRLKCESGKMKEMSDAEVBE 120
 OY 121 RRALIRKRSKERTGTPLGVGGLTEEDORMIRLMDAOKRTDPTFSHRKRNRLPGVLSS 180
 DB 121 RRALIRKRSKERTGTPLGVGGLTEEDORMIRLMDAOKRTDPTFSHRKRNRLPGVLSS 180
 OY 181 GCCLPESLAPSRERAAKSNQVAKDLCSIKVSLQRLGEGSVWNKPPADSGKETFSLL 240
 DB 181 GCCLPESLAPSRERAAKSNQVAKDLCSIKVSLQRLGEGSVWNKPPADSGKETFSLL 240
 OY 241 PHMADSTVFKGIIISPAVVISFRRDLPIEDOTSLKGAFAELCOLRFTVNAETGWE 300
 DB 241 PHMADSTVFKGIIISPAVVISFRRDLPIEDOTSLKGAFAELCOLRFTVNAETGWE 300
 OY 301 CGRLSTCLEDTAGCFQOOLLLEPMLEFMYMLKRLQLHEEYVLMQALSLFSPDRPGVLAHR 360
 DB 301 CGRLSTCLEDTAGCFQOOLLLEPMLEFMYMLKRLQLHEEYVLMQALSLFSPDRPGVLAHR 360
 OY 361 VVDOLQEQFAITTKSTIECKRNPQARHFLFKIMAMLTLSRSINAOHRLRIQDIHF 420
 DB 361 VVDOLQEQFAITTKSTIECKRNPQARHFLFKIMAMLTLSRSINAOHRLRIQDIHF 420
 OY 421 ATPLEMLFSGITGS 434
 DB 421 ATPLEMLFSGITGS 434
 OY 421 ATPLEMLFSGITGS 434
 DB 421 ATPLEMLFSGITGS 434
 RESULT 11
 ID Y42691
 AC Y42691; standard; Protein: 414 AA.
 AC Y42691;
 AC Y42691;
 DT 17-JAN-2000 (first entry)
 DT 17-JAN-2000 (first entry)
 DE Human pregnane X receptor (hPXR).
 XX
 XX Human; nuclear receptor; pregnane X receptor; PXR; CYP3A4;
 KW cytochrome P-450 mono-oxygenase; drug interaction; hPXR.
 XX
 OS Homo sapiens.
 XX
 XX W09948915-A1.
 XX
 PD 30-SEP-1999.
 XX
 XX 26-MAR-1999; 99WO-US06737.
 XX
 XX 27-MAR-1998; 98US-0079593.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 XX
 XX Kilewer SA, Willison TM;
 XX
 XX WPI: 1999-601202/51.
 XX
 XX N-PSDB: Z07997.
 XX
 PT New human pregnane X receptor, used to identify specific modulators and
 PT agents that induce expression of cytochrome P-450 mono-oxygenase
 PT
 PS Claim 4; Fig 1A-D; 69pp; English.
 PS
 XX
 XX The invention provides an isolated human nuclear receptor (designated
 CC pregnane X receptor, PXR) that binds to a cytochrome P-450 mono-oxygenase
 CC (CYP) promoter. The hPXR is used to identify its specific modulators,
 CC and compounds that induce CYP3A4 expression (i.e. to identify drug
 CC interactions, since CYP3A4 is involved in many biotransformations of
 CC drugs). The modulators are potentially useful for associating particular
 CC diseases and conditions with PXR and for treating such conditions.

PT	New hummane X receptor, used to identify specific modulators and
PT	agents that induce expression of cytochrome P-450 mono-oxygenase -
XX	
PS	Example 6; Page 37; 69pp; English.

pregnane X receptor, PXR) that binds to a cytochrome P-450 mono-oxygenase (CYP) promoter. The hpxr is used to identify: its specific modulators, and compounds that induce CYP3A4 expression (i.e., to identify drug interactions since CYP3A4 is involved in many biotransformations of

CC antibodies raised against hpxr can be used for determination and
CC purification of hpxr. The present sequence represents a histidine-6
CC tagged partial pXr (His6-pXr) sequence.

Query Match	69.2%	Score 1585	DB 20	Length 316
Best Local Similarity	100.0%	Pred. No. 4.3e-149		
Matches 305: Conservative	0	Mismatches	0	Indels 0: Gaps
Sequence	316 AA:			

QY 130 SEPTGTPGCGVGLDEEQPMIRELMDAQMTFDTTTSHEKNERFLPEVLSSGCELPESIQ 189
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
12 settgctgpbyvgvltteeqgrmmatrelmdqmkftdttsnfknflpvvlssgelcpesiq 71
Db

QY 190 APSREBAAMSVQRKDCLSLKYSLOLRGEDSDVMNYPAPDASGGKEIFSLIPHMADMSY 249

Db 72 apareeakwsgytklcslkvslqlrtdgswvnykppadsgkelfsl1pmedmsty 131

250 MFGIISFAKVSISYFDLPIDPOISLTKGAPELCOLRFNTVNAETGTEGRLSYCLE 309

QY 132 mfgiisfakvsiyfdlpiedqslklygaafelcqlrlntvinaeqtwecrrisycle 191

QY 310 DTAGGGQOULLLEPMLKFMHMKKLDLHHEEYVLMQATISLSPSPRCVLDHRVVDOLQEOQ 369
 192 dtagsqgqlllepmlkfmhmkkldlheeeyvlmqatislspdrpylqhrvvdqlqeqf 251
 QY 370 ATLTKSTIECNRPQAHRLFLKTIAMLTETKRSINAOHTQRLRLDIDHFEATPLMQEFL 429

Db	252	atlkaylecnppqphnrlflfxlmamltetrsnaqhtqrllrlqqlhpfatpqlngelf	311
QY	430	GIRGS 434	
Db	312	gtrgs 316	

	RESULT	13
	ID	R98521
	XX	R98521 standard; Protein; 386 AA.
	MD	
	DOESNT	

AC	R692L1;
XX	
DT	14-NOV-1996 (first entry)
DE	Xenopus orphan receptor 6.
XX	
XX	
XX	Vitamin D receptor 6; VDR-6, steroid receptor, vitamin D,

NM		Location/Qualifiers
KW	hydroxybenzoate; mercaptobenzoate; aminobenzoate.	
RN		
XX	Xenopus laevis.	
OS		
XX		
Key		
FH	37 102	
Dominant		

FT	DNA_binding_domain
FT	/label=183..386
FT	/label=Ligand_binding_domain
XX	
XX	
PX	
MO9622390-A1.	

Query Match 69.2%; Score 1585; DB 20; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 130 SERTGTPAGVGLTEBQNMIRELMDQKTEFTDTTSHKRNFLPYVLSSGCELPESIQ 169

Db 12 seetgqbpdygglteeqgmmirelmdqmtftdtshkfnflpyvlssgcelpesiq 71

QY 190 APSREBAAMSOVKRDLCSLKYSIQLRGEDGSVMNKPAPADSGKELTSLIPMADMSY 249

Db 72 apreeaakwqyrkdlcslkvsrlqjredssvwnypnpadsgskelfslpimadmsty 131

Qy 250 MFKGISFAKVISYERDUPIEDOISILKGAPELCOLFNTVNAETGTCGRSLCYCLE 309

Db 132 mfkglstafavlsyfrldpiedqslkkgaafeqlrlfntvnaetgwcgrslscle 191

QY 310 DTFGGQQLLEPMNKKEHYMKKKIQLHEEYVLMQASISLSPDPGVLGHRYVDLQEOEP 369

Db 192 dtagcfqgdllepmlkfhymkkqlpheeeylmqaslsfspdpyvlqhrvvddqlqef 251

QY 370 AILKSTIECNRPQRAHRELFLKIAMLTETLSINAGHTQRLRLIQDIHFATPLMQELF 429

Db	252	atlkxyleonprqpehrflflkxmamtelrsinaqhtqrllrrigqhhpfacpplmgelf	311
OY	430	GIrGS 434.	
Db	312	grrgs 316	

RESULT	13
R98521	
ID	R98521 standard; 386 AA.
XX	
AC	R98521;

XX	14-NOV-1996 (first entry)
DT	
XX	
DE	Xenopus orphan receptor 6.
XX	
KW	Xenopus orphan receptor 6; XOR-6; steroid receptor; vitamin D; receptor

Accession	Key	Location/Qualifiers
AM	Hydroxybenzoate	mercaptobenzoate; aminobenzoate.
XX		
XX	Xenopus laevis.	
OS		
XX		
PH	Key	Location/Qualifiers
FT	Domain	37..102
XX		7-thiol nuc binding domain

[illegible]

PF 16-JAN-1996; 96WO-US00058.
 XX
 PR 17-JAN-1995; 95US-0374445.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Blumberg B, Evans RM, Umeson K;
 XX
 DR WPI; 1996-354546/35.
 DR N-PSDB; 736499.
 XX
 PT DNA encoding receptor polypeptide responsive to hydroxy, mercapto or
 PT amino benzoate(s) - useful to regulate gene transcription
 PS
 PS Claim 4; Page 27-28; 42pp; English.
 CC Xenopus orphan receptor 6 (XOR-6) (R98521) is a new member of the
 CC steroid receptor superfamily, characterised as being responsive to
 CC the presence of hydroxy, mercapto or amino benzoate(s) and as
 CC regulating the transcription of associated gene(s). It shows 73%
 CC identity in the DNA binding domain, and 42% identity in the ligand
 CC binding domain, to the human vitamin D receptor. Recombinant XOR-6
 CC can be expressed in animal cells; a cDNA clone (736499) coding for
 CC XOR-6 has been isolated. The recombinant XOR-6 may be used to
 CC regulate gene transcription or to raise antibodies of diagnostic
 CC or therapeutic appln.
 CC
 SO Sequence 386 AA;

Query Match 42.8%; Score 979.5; DB 17; Length 386;
 Best Local Similarity 48.6%; Pred. No. 6.8e-89;
 Matches 202; Conservative 60; Mismatches 105; Indels 49; Gaps 9;

QY 18 EETESVPGKPSVNADEEYGGPQICVCGDKAGYHFNWTCGCGCFRRAKRNRARC 77
 DB 14 EEEEDASNSCGTGEDDDGDPKICACGDRATCYHFNAMTCGCKGCFRRAKRNRARC 73
 QY 78 PFRKGCETTRKTRROCOACRLKCKESGKMKEMINSDEAVERALRK-KSERGTQ 136
 DB 74 PL-qnsclvknrthqecrlkcdlqmrkclmsdaaveqrralkrkhlkrlpt 132
 QY 137 PLGVGGLTEEQRMIRLEMDQMKFTDTFSHFKNRRLPGVLSGCELPESIQAPSRREA 196
 DB 133 ppgga-slipeqghflqtlyvghntkctfdnfctsknfr-----plr--- 171
 QY 197 AKMSQVRKDLCSLKVSLQLRGDSVWNTKPPADSGGKEIFSLPHMADMTYFKGIIS 256
 DB 172 -----rsedpr---qepqats---seafimlphladietylmikglls 207
 QY 257 FAKVSYFEDLPIDEOISLKGAFELCOLRNTVFNAETGWEGGRISYCLEDT-AGCF 315
 DB 208 fakmlpytklsldedqalixgsaevaviftnlvnsdntwecgpfctydedmflagf 267
 QY 316 QQLLEPMLKFRHYMLKQLLHEEYVLMQALSLFSPDPGVQLQHRVVDQLQOFAITLKS 375
 DB 268 rqlfleplvrlhmrklnvgeeyemmaalsifasyprydcwckikqlghalaltkd 327
 QY 376 YTECNR-POPARHFLPLKIMAMLTSLRSTNAOHTO--RLRQIDIRP-ATPLMOELFG 430
 DB 328 fidesgrpsppqrlllypkimecltelrtvndhskqllelwdlqdeaplmrevfg 383

RESULT 14
 W94623 standard; Protein; 423 AA.
 AC W94623;
 XX
 DT 29-APR-1999 (first entry)
 XX
 DE Rat vitamin D receptor protein VDR0.

KM Vitamin D receptor; VDR; bone density; retinoic acid derivative;
 KM steroid; bone calcium regulator; immunosuppressant; anticancer.
 XX
 OS Rattus sp.
 XX
 PN MO9856908-AL.
 PD
 PD 17-DEC-1998.
 PE
 PE 13-JUN-1997; 97WO-JP02052.
 XX
 PR 13-JUN-1997; 97WO-JP02052.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Kato S, Ueno K;
 XX
 DR WPI; 1999-080898/07.
 DR N-PSDB; X16606.
 XX
 PT Gene for vitamin D receptor isoform protein which blocks vitamin D
 PT signal pathway - and production of recombinant isoform protein using
 PT it, for bone density assay and for screening compounds for vitamin D
 PT activity.
 PS
 PS Example 1; Fig 1; 47pp; Japanese.
 CC
 CC The present invention describes rat vitamin D receptor (VDR) isoform
 CC protein VDR1. The present sequence represents rat VDR0. VDR1 differs
 CC from the canonical form of VDR (VDR0) by lacking the amino acid sequence
 CC encoded by exon 9, but instead substitutes a short sequence
 CC (GREGREELRDLGVGCE) in the rat protein) encoded by the 5'-end of intron
 CC 8. VDR1 has a dominant negative effect on the vitamin D signalling
 CC pathway. The isoform protein can be used for determining bone density,
 CC and for the screening of compounds (e.g. steroids and retinoic acid
 CC derivatives) for vitamin D activity (e.g. as bone calcium regulators,
 CC immunosuppressants or anticancer agents).
 CC
 SO Sequence 423 AA;

Query Match 35.0%; Score 801; DB 20; Length 423;
 Best Local Similarity 42.0%; Pred. No. 4e-71;
 Matches 172; Conservative 75; Mismatches 135; Indels 28; Gaps 9;

QY 38 PQCRCVGGDAATGYHFNWTCGCGCFRRAKRNRARCPRKGCETTRKTRROCOAC 97
 DB 21 plicvcgdattgfhnamtccecgkgyffrrsmrkalfcpf-ngdcrltkdnrncqgc 79
 QY 98 RLKRCLESGMKKEMINSDEAVERALRK-KSERGTQPLGVGGLTEEQRMIRLEMDA 157
 DB 80 rtkrcvdlgmkeflltcddevqgkrlmkrkeeealksalrpk-lseeqghlallida 138
 QY 158 QMKFTDTFSHFNFRLPGVL--SSGCELPESIQAPSRREAQMSQVRKDLCSLKV- 211
 DB 139 jhktydptydfidfprrymdsgtsysjpr-----plsfsgnsasssdlyctsdmme 194
 QY 212 -----SLQLRGDSVWNTKPPADSGGKEIFSLPHMADMTYFKGIISFAKVISYFED 266
 DB 195 psqfsmldngesd-----dpsvltldleplsmplhadiavyslqkvigfahmipgfrd 249
 QY 267 LPIDEOISLKGAFELCOLRNTVFNAETGWEGGRISYCLEDT--AGCGOQLLEPM 323
 DB 250 ltsddqvlvixsalaevlmtmrngsfctmdmavedcgsgdykdvctvskaghtellepl 309
 QY 324 LKFRHYMLKQLLHEEYVLMQALSLFSPDPGVQLQHRVVDQLQOFAITLKSYTECNRPQ 383
 DB 310 lkfgvylkrlnlneehvllmalclsvsdprrygdaklvealqdrtsnltqcytcrhpp 369
 QY 384 PAHREFLKIMAMLTSLRSTNAOHTO--RLRQIDIRP-ATPLMOELFG 430
 DB 370 pgsghlyakmqlkladlrslneehskysrlsfqpsnsmklplvlevfg 419

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RESULT 15
ID W47509 standard; Protein; 423 AA.
XX AC W47509;
XX DT 26-JUN-1998 (first entry)
XX DE Rat vitamin D receptor (VDR0).
XX XX
XX Rat; vitamin D receptor; isoform protein; VDR1; VDR0; diagnosis;
XX dominant negative receptor; signal transmission channel;
XX bone density disorder; screening.
XX OS Rattus rattus.
XX XX
XX Key Location/Qualifiers
XX FT Misc-difference 360 /note="encoded by CAG"
XX FT
XX FN W09747172-A1.
XX XX
XX PD 18-DEC-1997.
XX XX
XX PE 10-JUN-1997; 97WO-IB00947.
XX PR 10-JUN-1996; 96JP-0194179.
XX XX
XX PA (CHUS ) CHUGAI PHARM CO LTD.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PI Kato S, Ueno K;
XX DR WPI; 1998-051917/05.
XX DR N-PSDB; V03129.
XX XX
XX PT DNA encoding a vitamin D receptor isoform protein - useful for bone
XX activity
XX PT
XX PS Disclosure; Fig 1; 46pp; Japanese.
XX CC
XX CC A novel cDNA sequence encodes the rat vitamin D receptor isoform
XX CC protein (VDR1). The isoform differs from the normal receptor
XX CC (VDR0), which comprises the present sequence, in having the
XX CC vitamin D response element curtailed by 86 residues, and having an
XX CC extra 19 residues inserted at the C-terminal of this element. It
XX CC acts as a dominant negative receptor in the vitamin D signal
XX CC transmission channel.
XX CC The isoform protein can be used to diagnose bone density disorders,
XX CC and screen for substances having potential vitamin D-like activity.
XX SQ Sequence 423 AA;

Query Match 34.8%; Score 798; DB 19; Length 423;
Best Local Similarity 42.0%; Pred. No. 7.9e-71;
Matches 172; Conservative 74; Mismatches 136; Indels 28; Gaps 9;

QY 38 POICVCGDKATGYHFNMTCEGCKGFFRRAMKRNARLRCPPRGACETTRKTRROCOAC 97
DB 21 pricvcgdratgfhnamtcegcgkffrramkraltcfp-ngdcritkdnrrrhqac 79
QY 98 RLRKCLSGMKKEMTMSDAVEERRALIKRKSEKRTGTQPLGVOGLTEQRMTRRLMDA 157
DB 80 rlrkcvdigmhkeflltdeevqirkemlmkkeealxdsirpk-lseegqhliallida 138
QY 158 QMKTEDTFSHKKRNLPGVL--SSGCELPESLQAPSREAAKMSQVAKDCSLKV---- 211
DB 139 hnktydpcyadrditprrmdgsrgyspr---plstfsgnsssssdlyttsldme 194
QY 212 -----SLQLRGEDGSVMWTKPPADSGGKEIFSLPHMADMSTYMKGIISPAKVIYSFRD 266

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DB 195 psgfsmldngesd-----dbpsvldlsplsmldpladlvsyqkylgfkamipgrfd 249
QY 267 LPRIEDISLLKGAAPFLCOLRENTVFNMAETGWECEGRUSYCLEEDF--AGGRQQLLEPM 323
DB 250 ltsddqivllksalevlnlrngsfnddmawdcsgdqxydvldvskaghtllellep1 309
QY 324 LKPFYMLKKLOJHEERYVMOAISLSPDPKGVLOHRYVDOLQEQFATLKSIECNRPQ 383
DB 310 ikfvgliklnlheeenvlmaiclvspdrpyvqakivealqdarlsntltgtytrcrhnp 369
QY 384 PAHRFLFKIMAMLTSLRSINAOHTQ--RLLRIDIHFP-ATPLMOELFG 430
DB 370 psgnqlyakmiglkladrlslnesksqyslsfqpensmkltpvlvlfvg 419

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Search completed: February 18, 2001, 14:29:39
Job time: 8216 sec

Db 11 CVCAGDQATGTHFNALTCBCKGFFRRVSKSIGPTCEP-AGSCVSKTORRHCPCARLQ 69
 QY 101 KCLESQMKKIMSDAVERERALLRKKSERTGTPLGVQGLTEORMMIRELMDAQM 160
 Db 70 KCLDAGMRKMDILSAELALBRKAQARRAQPTPVQ-----LSKQELINTLLGAHTR 123
 QY 161 TPDTSHEKFRPLPGVLSGCELPESLQAPSEBAKMSQVRKDLCSLKSVLQRGEDG 220
 Db 124 HMGTFEQFQVFRPAHLFIHQ-PLPTLAP----- 153
 QY 221 SWNNKRPADSGKEIFSLPHMADSTYMGKIIISFAKVISYFRDLPTEODISILKGA 280
 Db 154 -----VPLTFHFDINTFMVLQVLFKTDLPVRSPLIEDQISILKGA 198
 QY 281 FELCOLRNTVFNAGTWEBCGRSLCYLEDTAG-GFOQLLEPMLKFHYMLKRLQHEE 339
 Db 199 VEICHTVANTTFCLOTQNLGCPRLRTIEDGARVGFVEFLFELFHGTLKRLQLOPE 258
 QY 340 YVLMQALISFSPDRPGVLAHRVVDLQEQFAITLKSIECNRPQPAHREFLKIMAMTE 399
 Db 259 YVLLAAMALFSPDRPGVQORDEIDQEQEMALTIQSYKQQRPRDRPFLVAKLIGLAE 318
 QY 400 LRSINAOHQRLRIODIHPEATPLMOEL 428
 Db 319 LRSINEAYGYQIOHIGLSAM-MPLLOEI 346

RESULT 2

US-08-458-686-10
 ; Sequence 10, Application US/08458686
 ; Patent No. 5710017

GENERAL INFORMATION:

APPLICANT: David D. Moore et al.
 TITLE OF INVENTION: CAR RECEPTORS AND RELATED
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458,686

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/843,350

FILING DATE: February 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Paul T. Clark

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/126001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 348

TYPE: amino acid

STRANDEDNESS: N/A

TOPOLOGY: Linear

Query Match

33.5%, Score 768; DB 1; Length 348;

Best Local Similarity 42.2%; Pred. No. 4,1e-68;
 Matches 164; Conservative 62; Mismatches 109; Indels 54; Gaps 6;
 QY 41 CVCAGDQATGTHFNALTCBCKGFFRRVSKSIGPTCEP-AGSCVSKTORRHCPCARLQ 100
 Db 11 CVCAGDQATGTHFNALTCBCKGFFRRVSKSIGPTCEP-AGSCVSKTORRHCPCARLQ 69
 QY 101 KCLESQMKKIMSDAVERERALLRKKSERTGTPLGVQGLTEORMMIRELMDAQM 160
 Db 70 KCLDAGMRKMDILSAELALBRKAQARRAQPTPVQ-----LSKQELINTLLGAHTR 123
 QY 161 TPDTSHEKFRPLPGVLSGCELPESLQAPSEBAKMSQVRKDLCSLKSVLQRGEDG 220
 Db 124 HMGTFEQFQVFRPAHLFIHQ-PLPTLAP----- 153
 QY 221 SWNNKRPADSGKEIFSLPHMADSTYMGKIIISFAKVISYFRDLPTEODISILKGA 280
 Db 154 -----VPLTFHFDINTFMVLQVLFKTDLPVRSPLIEDQISILKGA 198
 QY 281 FELCOLRNTVFNAGTWEBCGRSLCYLEDTAG-GFOQLLEPMLKFHYMLKRLQHEE 339
 Db 199 VEICHTVANTTFCLOTQNLGCPRLRTIEDGARVGFVEFLFELFHGTLKRLQLOPE 258
 QY 340 YVLMQALISFSPDRPGVLAHRVVDLQEQFAITLKSIECNRPQPAHREFLKIMAMTE 399
 Db 259 YVLLAAMALFSPDRPGVQORDEIDQEQEMALTIQSYKQQRPRDRPFLVAKLIGLAE 318
 QY 400 LRSINAOHQRLRIODIHPEATPLMOEL 428
 Db 319 LRSINEAYGYQIOHIGLSAM-MPLLOEI 346

RESULT 3

US-07-843-350C-10
 ; Sequence 10, Application US/07843350C
 ; Patent No. 5756448

GENERAL INFORMATION:

APPLICANT: David D. Moore et al.
 TITLE OF INVENTION: CAR RECEPTORS AND RELATED
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/843,350C

FILING DATE: February 26, 1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Paul T. Clark

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/126001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 348

TYPE: amino acid

STRANDEDNESS: N/A

Query Match

33.5%, Score 768; DB 1; Length 348;


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      ZIP: 07065-0907
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/330,518
      FILING DATE:
      CLASSIFICATION: 435
      ATTORNEY/AGENT INFORMATION:
      NAME: Dolan, Catherine A.
      REGISTRATION NUMBER: 36,502
      REFERENCE/DOCKET NUMBER: 19316
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (908) 594-4283
      TELEFAX: (908) 594-4720
      INFORMATION FOR SEQ ID NO: 2:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 461 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      HYPOTHEICAL: NO
      ANTI-SENSE: NO
      US-08-330-518-2
  
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Query Match      21.7%; Score 498; DB 1; Length 461;
Best Local Similarity 29.0%; Pred. No. 3.6e-41;
Matches 126; Conservative 86; Mismatches 125; Indels 98; Gaps 14;
  
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QY 37 GPOICVCGDKATGYHFNWTCGCGFFRRAMKRNALRCFRR-KGACEITRRKRCQ 95
DB 83 GHELCRVCGDKAGSFHYNVSCGCGFFRRSVRGARRVACRGGTCOMDAFMRKCQ 142
QY 96 ACRLKRCLESGMKKEMIMSDAEVERRALIKRKSERTGTQ--PLGVQG----- 142
DB 143 QCRLRCKEAGMEQCVLSSEQIRKK--IRKQOQESQSOSQSPVGGSSSSASGPGA 200
QY 143 -----LTFEQRMIRELMDAOKTFDTTFSHKNRFLPGVLSGCE 183
DB 201 SPGSEAGSQSGEGEGVQLTAQCEIMIQLVAAQLQCNKRFS----- 244
QY 184 LPESIQAPSEBAKKSQVRKDCSLKVSQLRGEGSVWNNKPPADSGKRLFSILPHM 243
DB 245 -----DQKVTWMP-----LQAD-----PQSRDAQQRFA--HF 271
QY 244 ADMSTYFNGIISFAKVISYFRDLPIEDQISLLKGAFAELCOLRNTVFNATGTWEC-- 301
DB 272 TELAIISVQELVDFAKOVGFQLRGREDIALKASTIEIMLEFARRNHEIT--ECIT 328
QY 302 --GRLSYCLEDD-TAGGFQOLLEPMLEKHYMKKIQLEHEEYVLMQALSLSPDRPGVLQ 358
DB 329 FLKDFTYSDDEHRAQLQVEFINPIFEFSRARRRLGLDDEAYALLAINIFADBPVQCE 388
QY 359 HRVVDQLOEQPALTTSYIECNRPQAPAHFPLFKIAMMTELRSINAQHTQL--LRIOD 416
DB 389 PGRVVALQOQPYEVALSTYRIKRPQDQLR--FPRMLKLVSLRTLSVSHSEQVFLRLQD 446
QY 417 IHPFATPLMQELFGI 431
DB 447 --KKLPPLLSSEIMDV 459
  
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RESULT 6
US-08-330-283-2
; Sequence No. Application US/08330283
; Patent No. 5679518
; GENERAL INFORMATION:
; APPLICANT: Friedmann, Eitan
; APPLICANT: Holloway, M. Katharine
  
```

```

      APPLICANT: Rodan, Gideon
      APPLICANT: Rutledge, Su Jane
      APPLICANT: Schmidt, Azriel
      APPLICANT: Vogel, Robert
      TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS
      NUMBER OF SEQUENCES: 5
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: Merck & Co., Inc.
      STREET: 126 East Lincoln Avenue
      CITY: Rahway
      STATE: New Jersey
      COUNTRY: US
      ZIP: 07065-0907
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patentin Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/330,283
      FILING DATE:
      CLASSIFICATION:
      ATTORNEY/AGENT INFORMATION:
      NAME: Dolan, Catherine A.
      REGISTRATION NUMBER: 36,502
      REFERENCE/DOCKET NUMBER: 19327
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (908) 594-4283
      TELEFAX: (908) 594-4720
      INFORMATION FOR SEQ ID NO: 2:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 461 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      HYPOTHEICAL: NO
      ANTI-SENSE: NO
      US-08-330-283-2
  
```

```

Query Match      21.7%; Score 498; DB 1; Length 461;
Best Local Similarity 29.0%; Pred. No. 3.6e-41;
Matches 126; Conservative 86; Mismatches 125; Indels 98; Gaps 14;
  
```

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QY 37 GPOICVCGDKATGYHFNWTCGCGFFRRAMKRNALRCFRR-KGACEITRRKRCQ 95
DB 83 GHELCRVCGDKAGSFHYNVSCGCGFFRRSVRGARRVACRGGTCOMDAFMRKCQ 142
QY 96 ACRLKRCLESGMKKEMIMSDAEVERRALIKRKSERTGTQ--PLGVQG----- 142
DB 143 QCRLRCKEAGMEQCVLSSEQIRKK--IRKQOQESQSOSQSPVGGSSSSASGPGA 200
QY 143 -----LTFEQRMIRELMDAOKTFDTTFSHKNRFLPGVLSGCE 183
DB 201 SPGSEAGSQSGEGEGVQLTAQCEIMIQLVAAQLQCNKRFS----- 244
QY 184 LPESIQAPSEBAKKSQVRKDCSLKVSQLRGEGSVWNNKPPADSGKRLFSILPHM 243
DB 245 -----DQKVTWMP-----LQAD-----PQSRDAQQRFA--HF 271
QY 244 ADMSTYFNGIISFAKVISYFRDLPIEDQISLLKGAFAELCOLRNTVFNATGTWEC-- 301
DB 272 TELAIISVQELVDFAKOVGFQLRGREDIALKASTIEIMLEFARRNHEIT--ECIT 328
QY 302 --GRLSYCLEDD-TAGGFQOLLEPMLEKHYMKKIQLEHEEYVLMQALSLSPDRPGVLQ 358
DB 329 FLKDFTYSDDEHRAQLQVEFINPIFEFSRARRRLGLDDEAYALLAINIFADBPVQCE 388
QY 359 HRVVDQLOEQPALTTSYIECNRPQAPAHFPLFKIAMMTELRSINAQHTQL--LRIOD 416
DB 389 PGRVVALQOQPYEVALSTYRIKRPQDQLR--FPRMLKLVSLRTLSVSHSEQVFLRLQD 446
  
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OY 417 IHPFAPLMQELFCI 431
||:|:|:
DB 447 --KKLPPLSEIMDV 459

RESULT 7
US-08-646-248-2
Sequence 2, Application US/08646248
Patent No. 5939372

GENERAL INFORMATION:

APPLICANT: Friedman, Eitan

APPLICANT: Holloway, M. Katharine

APPLICANT: Rodan, Gideon

APPLICANT: Rutledge, Su Jane

APPLICANT: Schmidt, Azriel

APPLICANT: Vogel, Robert

TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 East Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: US

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/646,248

FILING DATE: 14-MAY-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/330,283

FILING DATE: 27-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Dolan, Catherine A.

REGISTRATION NUMBER: 36,502

REFERENCE/DOCKET NUMBER: 19327

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-4283

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 461 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-646-248-2

Query Match 21.7%; Score 498; DB 2; Length 461;

Best Local Similarity 29.0%; Pred. No. 3,6e-41;

Matches 126; Conservative 86; Mismatches 125; Indels 98; Gaps 14;

OY 37 GPQICVCGDKATGYHFNWTCGCGKGFRRARNAALRCPPR-KGACETTRKTRQCO 95

DB 83 GHLCVCGDKATGYHFNWTCGCGKGFRRARNAALRCPPR-KGACETTRKTRQCO 142

OY 96 ACRLRCLESGMKKEMIMDSDEAVERBALIKRKSTRTGTQ--PLGVG----- 142

DB 143 QCLRLRCLESGMKKEMIMDSDEAVERBALIKRKSTRTGTQ--PLGVG----- 200

OY 143 -----LTEORAMIRHMDAOKMTFTDTPSHKRNRLRGVLSGCE 183

DB 201 SPGSGEAGSGSGEGEVOLTAQELMTQOLVNAQLOCKNRSS----- 244

OY 184 LPESLAPSRHEAAKWSQVRRKDLCSLKVSLQRLGDEGVSVMNKKPPADSGKEIFSLPHM 243

DB 245 -----DCKVTPWP-----LGAD-----POSROARQORFA---HF 271

OY 244 ADMSTWNGKIISEFAVISYERDLPIDQISLKGAFELCOLRENTVNAETGMEC-- 301

DB 272 TETALISVQETIDPAQVQVEFLQGREDOIALKASTIEMLETARRKNHET---ECIT 328

OY 302 --GRLSYCLSD--TAGGFOOLLEPMKLFYMLKKLOLHEEYVLMQALISFSPDRGVLO 358

DB 329 FLNDFTYSKDFRAGLQVEEFINPIEFSSRAMRRLGLDAEYALLAINIFSDARNVGE 388

OY 359 HRVVDLOECFAITLKSIECNRPQAHRLFLKIMAMTELRSINAOITRL--LRID 416

DB 389 PGREVALQCFYVALLSYTRIKRPQOLR--FPRMLKLVSRTLSVSHSEQVAFALRLD 446

OY 417 IHPFAPLMQELFCI 431

DB 447 --KKLPPLSEIMDV 459

RESULT 8
PCT-US95-13924-2
Sequence 2, Application PC/TUS9513924

GENERAL INFORMATION:

APPLICANT: Friedman, Eitan

APPLICANT: Holloway, M. Katharine

APPLICANT: Rodan, Gideon

APPLICANT: Rutledge, Su Jane

APPLICANT: Schmidt, Azriel

APPLICANT: Vogel, Robert

TITLE OF INVENTION: METHOD FOR FINDING RECEPTOR POTENTIATORS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: 126 East Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: US

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13924

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Quagliato, Carol S.

REGISTRATION NUMBER: 35,330

REFERENCE/DOCKET NUMBER: 19327 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3809

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 461 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

PCT-US95-13924-2

Query Match 21.7%; Score 498; DB 4; Length 461;

Best Local Similarity 29.0%; Pred. No. 3,6e-41;

Matches 126; Conservative 86; Mismatches 125; Indels 98; Gaps 14;

OY 37 GPQICVCGDKATGYHFNWTCGCGKGFRRARNAALRCPPR-KGACETTRKTRQCO 95

DB 83 GHLCVCGDKATGYHFNWTCGCGKGFRRARNAALRCPPR-KGACETTRKTRQCO 142

OY 96 ACRLRCLESGMKKEMIMDSDEAVERBALIKRKSTRTGTQ--PLGVG----- 142

DB 143 QCLRLRCLESGMKKEMIMDSDEAVERBALIKRKSTRTGTQ--PLGVG----- 200

OY 143 -----LTEORAMIRHMDAOKMTFTDTPSHKRNRLRGVLSGCE 183

DB 201 SPGSGEAGSGSGEGEVOLTAQELMTQOLVNAQLOCKNRSS----- 244

OY 184 LPESLAPSRHEAAKWSQVRRKDLCSLKVSLQRLGDEGVSVMNKKPPADSGKEIFSLPHM 243

Db 83 GHELCRCVCGDKRAGFHNVLSCGCGKGFRRSVNGARVACRGGTGQMDAFRRKQ 142
 QY 96 ACRLKRCLESGMKKEMINSDAEVERRALIKRKSEKGTG---PLGVQ----- 142
 Db 143 QCRKCKEAGMRKQCVLSEEDIRKK--IRKQOQESQSQSVGVGSSSSASGPGA 200
 QY 143 -----LTEQRMIRELMDAQMTFTDTSFKKFRPLGVLSGCE 183
 Db 201 SPGSEAGSQSGSEBGVLTAAQELMQLVAQLOCNKRSFS----- 244
 QY 144 LPESLDAPSRERAAKWSQVRKDLCSLKVSLQLRGDSVWYKPPADSGGKTFSLPHM 243
 Db 245 -----DQPVTPWP-----LGAD-----PQSRARQORFA---HF 271
 QY 244 ADMSTYMGKIIISFAKVISYFRDLPEDQISLKGAFELQLRNTVFNATGTWEC-- 301
 Db 272 TELATISVOEYDFAKQVGFLOLGRDQIALKASTEIMLETARRYNHET---ECIT 328
 QY 302 --GRLSYCLD--TAGGFQOLLLEPMLEKHYMLKQLHEEYVLMQALSLFSPDRPGYLQ 358
 Db 329 FLKDFYSKDDPHRAGLQVEFINPIFEFSRAMRRLGLDADAYALLAINITSADRPVQ 388
 QY 359 HRVVDQLOEQFALTKSTIECNRPQARHFLFLKIMAMLTLSRINAOHTQRL--LRQD 416
 Db 389 PGRVEALQOPYEVALSTYRIKRPQDQLR--FPRMLKVLSTLTSVSHSQVAFALRLQD 446
 QY 417 IHFFATPLMOELFGI 431
 Db 447 --KKLPPLSEIMDV 459

RESULT 9

PCT-US95-13931-2
 Sequence 2, Application PC/TUS9513931

GENERAL INFORMATION:

APPLICANT: Friedmann, Eitan

APPLICANT: Holloway, M. Katharine

APPLICANT: Rodan, Gideon

APPLICANT: Schmidt, Azriel

APPLICANT: Vogel, Robert

TITLE OF INVENTION: USE OF RECEPTOR POTENTIATORS

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESS: Merck & Co., Inc.

STREET: 126 East Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: US

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13931

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Quaglinato, Carol S.

REGISTRATION NUMBER: 35,330

REFERENCE/DOCKET NUMBER: 19316 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3809

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 461 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO
 PCT-US95-13931-2

Query Match 21.7%; Score 498; DB 4; Length 461;
 Best Local Similarity 29.0%; Pred. No. 3,6e-41;
 Matches 126; Conservative 86; Mismatches 125; Indels 98; Gaps 14;

QY 37 GPQICRYCGDKATGATYFNNWTCBGCGKGFRRAMKRNALRCFFR-KGACETRTKTRCQ 95
 Db 83 GHELCRCVCGDKRAGFHNVLSCGCGKGFRRSVNGARVACRGGTGQMDAFRRKQ 142
 QY 96 ACRLKRCLESGMKKEMINSDAEVERRALIKRKSEKGTG---PLGVQ----- 142
 Db 143 QCRKCKEAGMRKQCVLSEEDIRKK--IRKQOQESQSQSVGVGSSSSASGPGA 200
 QY 143 -----LTEQRMIRELMDAQMTFTDTSFKKFRPLGVLSGCE 183
 Db 201 SPGSEAGSQSGSEBGVLTAAQELMQLVAQLOCNKRSFS----- 244
 QY 184 LPESLDAPSRERAAKWSQVRKDLCSLKVSLQLRGDSVWYKPPADSGGKTFSLPHM 243
 Db 245 -----DQPVTPWP-----LGAD-----PQSRARQORFA---HF 271
 QY 244 ADMSTYMGKIIISFAKVISYFRDLPEDQISLKGAFELQLRNTVFNATGTWEC-- 301
 Db 272 TELATISVOEYDFAKQVGFLOLGRDQIALKASTEIMLETARRYNHET---ECIT 328
 QY 302 --GRLSYCLD--TAGGFQOLLLEPMLEKHYMLKQLHEEYVLMQALSLFSPDRPGYLQ 358
 Db 329 FLKDFYSKDDPHRAGLQVEFINPIFEFSRAMRRLGLDADAYALLAINITSADRPVQ 388
 QY 359 HRVVDQLOEQFALTKSTIECNRPQARHFLFLKIMAMLTLSRINAOHTQRL--LRQD 416
 Db 389 PGRVEALQOPYEVALSTYRIKRPQDQLR--FPRMLKVLSTLTSVSHSQVAFALRLQD 446
 QY 417 IHFFATPLMOELFGI 431
 Db 447 --KKLPPLSEIMDV 459

RESULT 10

US-08-342-411A-2

Sequence 2, Application US/08342411A

Patent No. 5639616

GENERAL INFORMATION:

APPLICANT: LIAO, Shutsung

APPLICANT: SONG, Ching

TITLE OF INVENTION: UNUSUAL NUCLEAR RECEPTOR

TITLE OF INVENTION: COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/342,411A

FILING DATE: 18-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KITCHELL, BARBARA S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: ARCD154

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-342-411A-2

Query Match	21.7%;	Score 496;	DB 1;	Length 460;
Best Local Similarity	29.08;	Pred. No. 5.6e-41;		
Matches 126;	Conservative 86;	Mismatches 125;	Indels 98;	Gaps 14;

[illegible]

US-08-333-358-8
US-08-333-358-8
Sequence 8, Application US/08333358
Patent No. 5571696
GENERAL INFORMATION:
APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONG Ms., ESTELITA S.
APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., TWE K.
APPLICANT: GIGHERE Ph.D., VINCENT MMN
APPLICANT: YAO Mr., TSO-PANG MMN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

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1 CURRENT APPLICATION DATA:
2     APPLICATION NUMBER: US/08/333,358
3     FILING DATE:
4     CLASSIFICATION: 435
5     PRIOR APPLICATION DATA:
6     APPLICATION NUMBER: US/07/761,068
7     FILING DATE:
8     ATTORNEY/AGENT INFORMATION:
9     NAME: Reltex Ph.D., Stephen E.
10    REGISTRATION NUMBER: 31192
11    REFERENCE/DOCKET NUMBER: P31 8936
12    TELECOMMUNICATION INFORMATION:
13    TELEPHONE: (619) 535-9001
14    TELEFAX: (619) 535-8949
15    INFORMATION FOR SEQ ID NO: 8:
16    SEQUENCE CHARACTERISTICS:
17        LENGTH: 440 amino acids
18        TYPE: amino acid
19        TOPOLOGY: linear
20    MOLECULE TYPE: protein
21
22 US-08-333-358-8

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Query Match	21.5%;	Score 491.5;	DB 1;	Length 440;
Best Local Similarity	29.7%;	Pred. No. 1.5e-40;		
Matches 127;	Conservative 85;	Mismatches 145;	Indels 71;	Gaps 12

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OY 18 EDESVYGRKSVADBEVGPICVGDGDKATGYHFNVMCEGCKGFFRANKRYAARLC 77
Db 68 EPPIPIRQKHKGRAPKMYLGNELSCVGDKASGHNIVLSCBEGCKGFFRSYKANHIC 12
OY 78 PFKGACEITRTKROCACRLKCSGMAKEMKMSDEAVEERALLIRKXSE----- 13
Db 128 -HSGHCEPMJTYRRKROCSRLKRCORAGMECEVLSEEDIRLTK--LKROEEOAHATS 18
OY 132 ---RTGPRIGVAGLNEEBRMJIREYMAOKKTDTEHSHFNKFLRGVLSGCELPESL 18
Db 185 LPPRRSPPILRLQUSPEBQJGKTELYVAOQCCRRSFS----- 22
OY 189 QASREBAAMWSOVRKDLCSLKVSLQJNGEDGSVMNKKPEADSGKEITSLPHNADMST 24
Db 224 ---DRUKVTPWMPAR-----DPSREARQGRFA---HFTELAI 25
OY 249 YMEKGITSRAKVIYSYRDLPIRIDOISLKGAEFLCOLRPNTYFN--AETGIVEGRLSY 30
Db 256 VSVQEIYDFKQJLPGFLQJLSREDOJALTKLTAIEYMLLESRRRNGESISITE-LKDFSY 31
OY 307 CLEDTA-GSGQOOLLEPYMLKPYMLKKTQLNEEYVLMQASISLSPDRBGVLQHRVDD 36
Db 315 NREDFAAGIQVEFIMPIYIEFSRAMELOQLDANAFALLIATSFSADRPRVQDQLOVEL 37
OY 366 QEOFAITLKSIECNRPQANRBEFLKLTAMVLELRSINQHTQRL--LRIDIHFAEP 42
Db 375 QHTVEVLAHYVSIINRPH--DLMPRPYMLKTVLSTLSVSEDOYFALRLD--KLEPP 43
OY 424 LMDELFCI 431
Db 431 LLSLSEIMDV 438

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RESULT 12
US-08-463-694-8
Sequence 8, Application US/08463694
Patent No. 5696233,
GENERAL INFORMATION:
APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGENSDORF Ph.D., DAVID J
APPLICANT: ONG MS., ESTELIRA S.
APPLICANT: ORO Ph.D., ANTHONY E.
APPLICANT: BORGMAYER Ph.D., TWE K.
APPLICANT: GIGUEURE Ph.D., VINCENT MNM
APPLICANT: YAO MR., TSO-PANG MNM
TITLE OF INVENTION: NOVEL RECEPTORS


```

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,694
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/761,068
FILING DATE: 17-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8936
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-694-8

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Query Match 21.5%; Score 491.5; DB 1; Length 440;
 Best Local Similarity 29.7%; Pred. No. 1.5e-40;
 Matches 127; Conservative 85; Mismatches 145; Indels 71; Gaps 12;

18 EDTSVPGKPSVNADEVEGPOICRVCGDKATGHNVTGCGKGFRRAMKRNARLC 77
 68 EPTETRPKRRKGPAPKMGNEICVCGDKASGFHYNLSCGCGKGFRRSYIKGAHYIC 127
 78 PFRKACETITRTROCOACRLKCLSGMKKEMSDAVERALIKRKSE----- 131
 128 -HSGGHCPCMDYMRKRCQCRKRCQAGMRBEVLSGEQITLKK--LKQDEEGAHATS 184
 132 ---RTGTOPLYOGLTREQRMIRLMDQMTPTTFSHKFNFLPGVLSGCELPESL 188
 185 LPPRRSSPOLLPOLSPQGLGMIETLVAAQQCNRRSF----- 223
 189 QAPSRSEAKKSVQRKDCSLKVSQLRGEGDSVNNYKPPADSGGKEITFSLPHMADMT 248
 224 ---DLRATVPMPAP-----DPHSREARQORFA--HFTETLAI 255
 249 YMFKGIISFAKVISYFRDLPIEDQISLKGAFELCOLRFTVFN--AETGTWECGRLSY 306
 256 VSVQIVDFPAQLPQGLQSLREDQIALKTSALTEYMLTETSRRTNPGSESTTF--LKDFSY 314
 307 CLEDEPA--GGFOOLLLEPMKFMMLKQLHEEEVYVLMQAISLSPSPDPGVLAQRVVQDL 365
 315 NREDPAKAGLOVEFTINPTFEFSRAMNELQLNDAPFALLIAISISADRPVNOQLOVERL 374
 366 QEQPAITLKSYIECNRPQAPRFLFLKTMAMULTELRISNAQHTORL--LRIQDIHPFATP 423
 375 QHTYEALHAYVSIHHPH--DRIMEPRMILKIVSLRTLSVSHQVVALRLQD--KKLP 430
 424 LMOELFGI 431
 431 LLSLTIWDV 438

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RESULT 13
US-08-694-501-8
Sequence 8, Application US/08694501
Patent No. 5710004
GENERAL INFORMATION:
APPLICANT: EVANS Ph.D., RONALD M.
APPLICANT: MANGELSDORF Ph.D., DAVID J.
APPLICANT: ONG M., ESTELITA S.
APPLICANT: ONG Ph.D., ANTHONY E.
APPLICANT: BORGMEYER Ph.D., UWE K.
APPLICANT: GIEBBER Ph.D., VINCENT NNN
APPLICANT: YAO M., TSO-PANG NNN
TITLE OF INVENTION: NOVEL RECEPTORS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: US
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,501
FILING DATE: 07-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/333,358
FILING DATE:
APPLICATION NUMBER: US/07/761,068
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8936
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-694-501-8

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Query Match 21.5%; Score 491.5; DB 1; Length 440;
 Best Local Similarity 29.7%; Pred. No. 1.5e-40;
 Matches 127; Conservative 85; Mismatches 145; Indels 71; Gaps 12;

18 EDTSVPGKPSVNADEVEGPOICRVCGDKATGHNVTGCGKGFRRAMKRNARLC 77
 68 EPTETRPKRRKGPAPKMGNEICVCGDKASGFHYNLSCGCGKGFRRSYIKGAHYIC 127
 78 PFRKACETITRTROCOACRLKCLSGMKKEMSDAVERALIKRKSE----- 131
 128 -HSGGHCPCMDYMRKRCQCRKRCQAGMRBEVLSGEQITLKK--LKQDEEGAHATS 184
 132 ---RTGTOPLYOGLTREQRMIRLMDQMTPTTFSHKFNFLPGVLSGCELPESL 188
 185 LPPRRSSPOLLPOLSPQGLGMIETLVAAQQCNRRSF----- 223
 189 QAPSRSEAKKSVQRKDCSLKVSQLRGEGDSVNNYKPPADSGGKEITFSLPHMADMT 248
 224 ---DLRATVPMPAP-----DPHSREARQORFA--HFTETLAI 255
 249 YMFKGIISFAKVISYFRDLPIEDQISLKGAFELCOLRFTVFN--AETGTWECGRLSY 306

Db 256 VSOEIVDPANQOLPGFLOJLSREDOIALKLTSAIEVMLLETSRRYNGSESITF-LKDFSY 314
QY 307 CLEDTA-GGFQOLLEPMLEKFKYMLKQLOHEEYVLMQAIISFSPDRGVLQHRVVDL 365
Db 315 NREDFAKAGLOVEFINIFEFSSRANMELQNDAEFALLIAISFSDRPNVODLOVERL 374
QY 366 QEOFAITLKSYIECNRPQAPARFLFKTAMLTSLRSINAQHTORL--LRIDIHPRATP 423
Db 375 QHTVEALHAYVSIHHPH--DRIMEPRLMKLVSLRTLSVSHQVVALRLQD--KKLP 430
QY 424 LMOELFGI 431
Db 431 LSEIMDV 438
RESULT 14
US-08-373-935-1
; Sequence 1, Application US/08373935
; Patent No. 5747661
; GENERAL INFORMATION:
; APPLICANT: Evans, Ronald M.
; APPLICANT: Mangelsdorf, David J.
; APPLICANT: Willy, Patricia J.
; TITLE OF INVENTION: IDENTIFICATION OF A DISTINCT
; TITLE OF INVENTION: RETINOID-RESPONSIVE PATHWAY AND USES THEREFOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373.935
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9894
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-4737
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-373-935-1
Query Match 21.5%; Score 491.5; DB 1; Length 447;
Best Local Similarity 29.7%; Pred. No. 1.5e-40;
Matches 127; Conservative 85; Mismatches 145; Indels 71; Gaps 12;

QY 189 QARSREBARWQVRKDCSLVSLQNGEDGSVNNYRPPADSGKEIFSLPHMADMT 248
Db 231 ---DRURVTFWPAAP-----DPHSNARQORFA---HFTELAI 262
QY 249 YMEGIISEFAKYSYFRDLPEDQISILKGAFFELCOLRNTVEN--AETITWECRLSY 306
Db 263 VSOEIVDPANQOLPGFLOJLSREDOIALKLTSAIEVMLLETSRRYNGSESITF-LKDFSY 321
QY 307 CLEDTA-GGFQOLLEPMLEKFKYMLKQLOHEEYVLMQAIISFSPDRGVLQHRVVDL 365
Db 322 NREDFAKAGLOVEFINIFEFSSRANMELQNDAEFALLIAISFSDRPNVODLOVERL 381
QY 366 QEOFAITLKSYIECNRPQAPARFLFKTAMLTSLRSINAQHTORL--LRIDIHPRATP 423
Db 382 QHTVEALHAYVSIHHPH--DRIMEPRLMKLVSLRTLSVSHQVVALRLQD--KKLP 437
QY 424 LMOELFGI 431
Db 438 LSEIMDV 445
RESULT 15
US-08-372-652-3
; Sequence 3, Application US/08372652
; Patent No. 5932699
; GENERAL INFORMATION:
; APPLICANT: Moore, David
; APPLICANT: Seol, Mongi
; APPLICANT: Choi, Hwang-Sik
; TITLE OF INVENTION: RETINOID X RECEPTOR-INTERACTING
; TITLE OF INVENTION: POLYPEPTIDES AND RELATED MOLECULES AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street, Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372.652
; FILING DATE: 13-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/246001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELE: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-372-652-3
Query Match 21.4%; Score 490; DB 2; Length 446;
Best Local Similarity 29.1%; Pred. No. 2.1e-40;
Matches 125; Conservative 84; Mismatches 128; Indels 92; Gaps 14;

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QY 96 ACRLKCLESGMKKIMMSDEAVEERRALIKRKSER-----TGTOP 137
Db 134 LRLRCKEAGMRBEOCVLSEEOIRKR--TOKOQOQPPPPSEPAASSSGRPAASPGTSE 191
QY 138 LGVQG-----LTEBQRMIRELMDAQMTFTTFSHKFNRLPGVLSGCELPESLQ 189
Db 192 ASSQSGEGEGIOLTAQELMIQOLVAQOLQCNKRFS----- 229
QY 190 APSREAAWQVQRKDLCSLKVSLQLRGDSVWNTKPPADSGGKEIFSLPHMADNMTY 249
Db 230 --DQPRVTPWP-----LGAD-----POSADARQORFA--HFTELAI 262
QY 250 MFKGISFAKVISYFRDLPIEDQISLNGAFELCOLRENTVFNAETGTWEC---GRLS 305
Db 263 SVOEIVDFAKQVPGFIQLRBDOIALKASTIEIMLQARRYNHE--ECITFLKDF 319
QY 306 YCLIED--TAGGFQOLLEPMUKFHYMLKTLQHEEYVLMQAISLSPDRPGVLOHRYDQ 364
Db 320 YSKDDEHRAGLQVEFINPIFEFSRAMRRLGLDADAEYALIALINISADRPNVQEPSRVEA 379
QY 365 LOEQFALITKSYTECNRPQPAHREFLFKIMAMTELRSINAQHTORL--LRJODIHPPAT 422
Db 380 LQOPVYBALISTYRIKRPQDQLR--FPRMLKIVSLRTLSVHSEGVFALRLQD--KRLP 435
QY 423 PLMQELFGEI 431
Db 436 PLTSEIMDV 444

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Search completed: February 18, 2001, 14:31:58
 Job time: 6201 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2001, 12:06:00 ; Search time 51.75 Seconds

(Without alignments)
270.834 Million cell updates/sec

Title: US-09-143-828-2
Perfect score: 2290
Sequence: 1 MEVPRKESNMHADFHCEDT.....QDIHPATPLMDELFCITGS 434

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Lasting first 45 summaries

Database: SwissProt_39

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2390	100.0	434	1	PXR_HUMAN
2	1779.5	77.7	431	1	PXR_MOUSE
3	1761.5	76	431	1	PXR_PAT
4	815.5	35.6	448	1	VDR_COTVA
5	815	35.6	451	1	VDR_CHICK
6	814	35.5	422	1	VDR_XENLA
7	801	35.0	423	1	VDR_RAT
8	792.5	34.6	422	1	VDR_MOUSE
9	789	34.5	424	1	VDR_BOVIN
10	789	34.5	427	1	VDR_HUMAN
11	768	33.5	448	1	NR13_HUMAN
12	729	31.8	358	1	NR13_RAT
13	725	31.7	358	1	NR13_MOUSE
14	498.5	21.8	445	1	NRH3_MOUSE
15	498	21.7	445	1	NRH2_HUMAN
16	496.5	21.7	445	1	NRH3_RAT
17	491.5	21.5	447	1	NRH3_HUMAN
18	489	21.4	446	1	NRH2_MOUSE
19	487	21.3	446	1	NRH2_RAT
20	455.5	19.9	395	1	THB_PAROL
21	450	19.7	369	1	THB_CHICK
22	450	19.7	461	1	THB_HUMAN
23	449	19.6	373	1	THB_BANCA
24	448	19.6	373	1	THB_XENLA
25	445	19.4	476	1	THB2_HUMAN
26	444.5	19.4	476	1	THB2_MOUSE
27	443	19.3	414	1	THB2_RAT
28	442	19.3	414	1	THB2_MOUSE
29	441	19.3	475	1	THB2_MOUSE
30	441	19.3	475	1	THB2_MOUSE
31	437	19.1	461	1	THB1_RAT
32	437	19.1	461	1	THB1_RAT
33	434	19.0	416	1	THA_PAROL

34	433.5	18.9	427	1	THA1_BRARE	O98867 brachydanio
35	432	18.9	878	1	ECR_DROME	P34021 drosophila
36	428	18.7	448	1	ROR2_HUMAN	P10826 homo sapien
37	427.5	18.7	458	1	RRA_XENLA	P51126 xenopus lae
38	427.5	18.7	550	1	ROR2_HUMAN	P51149 homo sapien
39	426.5	18.6	556	1	ECR_MANSE	P49883 manduca sex
40	425.5	18.6	408	1	THA_CHICK	P04625 gallus gall
41	425	18.6	455	1	ROR2_HUMAN	P22448 gallus gall
42	423.5	18.5	402	1	THA_APPRA	O42295 apendocytes
43	423.5	18.5	402	1	THA_APPRA	O42450 pygocelis
44	421.5	18.4	458	1	RRA_PYGAD	P18514 notophthalm
45	421.5	18.4	536	1	ECR_CHITE	P49882 chironomus

ALIGNMENTS

RESULT	ID	PXR_HUMAN	STANDARD	PRT	434 AA.
AC	075469				
DT	15-JUL-1999	(Rel. 38, Created)			
DT	15-JUL-1999	(Rel. 38, Last sequence update)			
DT	30-MAY-2000	(Rel. 39, Last annotation update)			
DE	ORPHAN NUCLEAR RECEPTOR PXR (PREGNANE X RECEPTOR) (ORPHAN NUCLEAR RECEPTOR PARL).				
GN	NR112 OR PXR.				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-LIVER:				
RX	MEDLINE-98395173; PubMed-9727070;				
RA	Lehmann J.M., Kckee D.D., Watson M.A., Willson T.M., Moore J.T.,				
RA	Kliwer S.A.;				
RT	"The human orphan nuclear receptor PXR is activated by compounds that regulates CYP3A4 gene expression and cause drug interactions.";				
RL	J. Clin. Invest. 102:1016-1023(1998)				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-LIVER:				
RX	MEDLINE-98445350; PubMed-9770465;				
RA	Bertilsson G., Heidrich J., Svensson K., Asman M., Jendeborg L.,				
RA	Sydney-Bachman M., Ohlsson R., Postlind H., Blomquist P.,				
RA	Berkestrand A.;				
RT	"Identification of a human nuclear receptor defines a new signalling pathway for CYP3A induction.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 95:12208-12213(1998).				
CC	- FUNCTION: ORPHAN RECEPTOR: ITS NATURAL LIGAND IS PROBABLY PREGNANE. BINDS TO A RESPONSE ELEMENT IN THE CYP3A4 GENE PROMOTER.				
CC	- SUBUNIT: FORMS A HETERODIMER WITH RXR.				
CC	- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).				
CC	- TISSUE SPECIFICITY: EXPRESSED IN LIVER, COLON, AND SMALL				
CC	INTESTINE.				
CC	- INDUCTION: ACTIVATED BY NATURALLY OCCURRING STEROIDS SUCH AS				
CC	PREGNENONE AND PROGESTERONE.				
CC	- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.				
CC	NRL SUBFAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL; AF061056; AAD05436.1; -				
DR	EMBL; AF084645; AAC64558.1; -				
DR	MIM; 603065; -				
DR	INTERPRO; IPR000324; -				
DR	INTERPRO; IPR000536; -				


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Db 1 MRPERNNHGLVOREADSVLEEP-INVDEEDGGIQCRCWGDKRANGYHFNVTCEGCK 59
Oy 63 GFFRFRAMKRNRLRCPFRKAGACEITRTKTRROCAARLFRKCLESGKKKMMISDAVEBR 122
Db 60 GFFRFRAMKRNRLRCPFRKAGACEITRTKTRROCAARLFRKCLESGKKKMMISDAVEBR 119
Oy 123 ALIRKKSERFGTOPLGVOCGLTEORRMTRBELMDOMKTFDTTSHFNRLPGVLSGC 182
Db 120 ALIRKKSERFGTOPLGVOCGLTEORRMTRBELMDOMKTFDTTSHFNRLPGVLSGC 179
Oy 183 ELPEISQAPSEEAARKSVKRCGLSARYSLORSGEDGSVWVVRPPADSGGKEIFSLPH 242
Db 180 ELPEISQAPSEEAARKSVKRCGLSARYSLORSGEDGSVWVVRPPADSGGKEIFSLPH 239
Oy 243 MADNSTYFNGIISFANVISYFNDLPIDEOISLNGAFLCOLFNFVFAETGTWECG 302
Db 240 LADSTYFNGIISFANVISYFNDLPIDEOISLNGAFLCOLFNFVFAETGTWECG 299
Oy 303 RLSCYEDTGGPGPOLLEPMLEKFNHMKKLOLHHEEYVLMQALISFDPDPVLOHRYV 362
Db 300 RLSCYEDTGGPGPOLLEPMLEKFNHMKKLOLHHEEYVLMQALISFDPDPVLOHRYV 359
Oy 363 DOLGEOFAITLKSYTECNRPPAHRELFLFKIMAMTELRSINAGHTORLRIODIHFEAT 422
Db 360 DOLGEOFAITLKSYTECNRPPAHRELFLFKIMAMTELRSINAGHTORLRIODIHFEAT 419
Oy 423 PLMOELFGIT 432
Db 420 PLMOELFSST 429

RESULT 4
VDR_COTJA ID VDR_COTJA STANDARD: PRT: 448 AA.
AC P49701;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, last sequence update)
DT 30-MAY-2000 (Rel. 39, last annotation update)
DE VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
GN VDR OR NR11.
OS Ccuturix coturix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Ccuturix.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CHORIOALLANTOIC MEMBRANE;
RX MEDLINE=95062315; PubMed=7972109;
RA Elarousat M.A., Prah J.M., Deluca H.F.;
RT "The avian vitamin D receptors: primary structures and their
RL origins."
Rt Proc. Natl. Acad. Sci. U.S.A. 91:11596-11600(1994).
CC -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
CC THE EXPRESSION OF HORMONE SENSITIVE GENES.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- ALTERNATIVE PRODUCTS: TWO FORMS (A AND B) ARE PRODUCED BY USE OF
CC ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NRI SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U12641; AA56725.1; ..
DR HSSP: P03372; 1HCQ.
DR INTERPRO: IPR000324; ..

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QY 224 NKPADSGGKIFSLPHMADSTYMEKGIISFAKVISYERDLPIDEDISLKGAFEL 283
 DB 242 NIEPH-----LPMPLHDLAVSISIOKIFAKMIPGRDLTADQIALKSSAIEV 294
 QY 284 COLPENTVNAETGWEGR--LSYCLEL-TAGFQOLLEPHKFKYMKKLOLHEEY 340
 DB 295 IMLNSOSFTWEDMSWTCGSNDKFKYSDVQACHSMLEPLVKFQVGRKKNLHEEH 354
 QY 341 VLMOAISLSPDRPGVLOHVRVDOLOFOFATLTKSYIECNRPORAHFPLFKIMLTEL 400
 DB 355 VLMAICILSPDRPGVODTSLVESIODRLSDILOTYIRCHHPGSGSLYAKMIQKLADL 414
 QY 401 RSTNAHQO--RLLRIDIHPE-ATPLMOELFG 430
 DB 415 RSLNEHSKQYRCLSFQPSHMOITPLVLEVF 447

RESULT 6
 VDR_XENLA STANDARD; PRT; 422 AA.
 ID VDR_XENLA 013124;
 AC 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
 GN VDR OR NR11.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RX MEDLINE-97307679; PubMed-9165021;
 RA Li Y.C., Bergwitz C., Jeppner H., Demay M.B.;
 RT Cloning and characterization of the vitamin D receptor from Xenopus
 laevis.
 RT Endocrinology 138:2347-2353(1997).
 RL -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
 CC THE EXPRESSION OF HORMONE SENSITIVE GENES.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: DETECTED IN ALL THE TISSUE EXAMINED. HIGHEST
 CC LEVEL IN SMALL INTESTINE AND SKIN
 CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT STAGE 13. INCREASES
 CC GRADUALLY AND PEAKS AT STAGE 57-61 THEN DECREASES TO THE LEVEL
 CC SEEN IN ADULT.
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NRI SUBFAMILY.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: U91846; AAB58585.1;
 DR INTERPRO: IPR000324;
 DR INTERPRO: IPR000336;
 DR INTERPRO: IPR001628;
 DR PFAM: PF00104; hormone_rec; 1.
 DR PFAM: PF00105; zf-C4; 1.
 DR PRINTS: PR00047; STROIDINGER.
 DR PRINTS: PR00350; VITAMINDR.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger.
 FT DNA_BIND 25 90 C4-TYPE ZINC FINGERS (TWO).
 FT ZN_FING 25 45 C4-TYPE.
 FT ZN_FING 61 85 C4-TYPE.

FT DOMAIN 91 188 HINGE.
 FT DOMAIN 188 422 LIGAND-BINDING.
 SQ SEQUENCE 422 AA: 48188 MW: C8A9F25414FEE9D5 CRC64;

Query Match 35.5% Score 814: DB 1: Length 422;
 Best local similarity 41.1%: Pred. No. 4e-58;
 Matches 172: Conservative 74; Mismatches 123; Indels 50; Gaps 10;

QY 38 POICRVCGDKATGYHFNWTCGKGFERRAMKRNARLCPFRKGCACETRTTRQOCAC 97
 DB 22 PRICGCGDKATGYHFNWTCGKGFERRAMKRNARLCPFRKGCACETRTTRQOCAC 80
 QY 98 RLKRLSGKKEMIMSDENVERBALIKKKSETGTOPAGVGLTEEQRMIRELMDA 157
 DB 81 RLKRCVDIGMKKEFLITDEEVORKNRKRSSEALSKESMRK-LSDEQOKMIDILLEA 139
 QY 158 QMKFTDTTSHKRNRLGVLSSGCELPESLQAPREBAKMSQVRKDCSLKYSLOLG 217
 DB 140 HKRTDTTYSDEKRR-----PPYRENVDFRRITR-----SSVHTG 178
 QY 218 ---EDGSWNKYPADS-----GKGE-IFSLPHMADSTYMEKGIIS 256
 DB 179 SPSEDSDFVTSPPDSEHGFASLFGQFEXSSMGKRGELSMPLHDLAVSISIOKIG 238
 QY 257 FAKVISYERDLPIDEDISLKGAFELCOLPENTVNAETGWEGR--LSYCLEL-TAG 313
 DB 239 FAKMIPGRDLTADQIALKSSAIEVIMLNSOSFTWEDMSWTCGSNDKFKYSDVQACH 298
 QY 314 GEOOLLEPKLKFHYMKKLOLHEEYVLMOAISLSPDRPGVLOHVRVDOLOFOFATL 373
 DB 299 GNNELLEPLVKFQVGRKKNLHEEHVLMAICILSPDRGLODKALVESIODRLSSTL 358
 QY 374 KSYTCNPPCAHNFLEFKIMTELKRSINAHQO--RLLRIDIHPE-ATPLMOELF 429
 DB 359 QYTIICKHPGSGSLYAKMIQKLADLRLSNEHSKQYRCLSFQPSHMOITPLVLEVF 417

RESULT 7
 VDR_RAT STANDARD; PRT; 423 AA.
 ID VDR_RAT P13053;
 AC 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
 GN VDR OR NR11.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-89071726; PubMed-2849110;
 RA Burmeister J.K., Wiese R.J., Maeda N., Deluca H.;
 RT "Structure and regulation of the rat 1,25-dihydroxyvitamin D3
 receptor."
 RT Proc. Natl. Acad. Sci. U.S.A. 85:9499-9502(1988).
 RL [2]
 RP SEQUENCE OF 58-423 FROM N.A.
 RX MEDLINE-88124963; PubMed-2829212;
 RA Burmeister J.K., Maeda N., Deluca H.F.;
 RT "Isolation and expression of rat 1,25-dihydroxyvitamin D3
 cDNA."
 RT Proc. Natl. Acad. Sci. U.S.A. 85:1005-1009(1988).
 CC -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
 CC THE EXPRESSION OF HORMONE SENSITIVE GENES.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC NRI SUBFAMILY.
 CC
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EMBL J04147; AAA41089.1; -
DR PIR: A31761; A31761.
DR PIR: A31367; A31367.
DR HSR: P03372; 1HCO.
DR TRANSFAC: T00882; -
DR INTERPRO: IPR000324; -
DR INTERPRO: IPR000536; -
DR INTERPRO: IPR001628; -
DR PFAM: PF00104; hormone_rec; 1.
DR PFAM: PF00105; zf-C4; 1.
DR PRINTS: PR00047; STEROIDFINGER.
DR PRINTS: PR00350; VITAMINDR.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
DR RECEPTOR: Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Phosphorylation.
FT DNA_BIND 24 89 C4-TYPE ZINC FINGERS (TWO).
FT ZN_FING 24 44 C4-TYPE.
FT ZN_FING 60 44 C4-TYPE.
FT DOMAIN 90 187 HINGE.
FT DOMAIN 188 423 LIGAND-BINDING.
SQ SEQUENCE 423 AA; 47813 MW; 1A0E519A9DCCE990 CRC64;

Query Match 35.0%; Score 801; DB 1; Length 423;
Best Local Similarity 42.0%; Pred. No. 4.5e-57;
Matches 172; Conservative 75; Mismatches 135; Indels 26; Gaps 9;

38 POICRVCGDKATGYHFNWATCEGCKGFFRRAMRNALRCFFPKGACITRTKTRCOAC 97
DB 21 PRIGCVGDKATGYHFNWATCEGCKGFFRRAMRNALRCFFPKGACITRTKTRCOAC 97
QY 98 RLKRCESGKMKEMIMSDAVERALIKRKSEKSTGTOPLGVOGLTEORMMIRELMDA 157
DB 80 RLKRCVDMGKKEFLITDEVOARKREIMKREELALDLSRPK-LSEEQHIIAIIILDA 138
QY 158 QMKEFDTTFSHKKNFLP-GVL-SSGCELPESIQAPSRERAAKWSQVRKDCISLKV- 211
DB 139 HKHTYPTIADPRFRPRVADSGSYSPR-PLTSSGSSSSSSSLTYSIDMME 194
QY 212 -----SLQKGEDESVNWKRPADSGKREIFSLPHVADSTYFKGIIIPAVYISFRD 266
DB 195 PSGRSNDLNGEDSD-----DPSVTLDLSPLSMLPHLADVSYSIOKVIQGFAMKIPGRD 249
QY 267 LPIDQISLKGAFELCOLRENTVFNNAETGTEGRLSYCLEDT---AGGFQOILLPEM 323
DB 250 LITSDQIVLKSSAIEVIMKSNOSFTMDMSWDCSGSDYKYDVTVDYKAGHTELEPL 309
QY 324 LKFMKLKQLOLHEEYVLMQALISLSPRPGVQLQHRVVDQLOEOPALTKSYTECNRPQ 383
DB 310 IKFOYGLKLLHBEHVLMAICIVSPDRGVODAKLVEAIDRLSNTLQTYRCRRHP 369
QY 384 PAHRFLKTKAMTELASINAGTO--RLRIDIRHF-ATPLMOELFG 430
DB 370 PSHQLYAKMIOKLADLSLNEHRSKORYSLSFQENSMKLTPLVLEVF 419

RESULT 8
VDR_MOUSE STANDARD; PRT; 422 AA.
AC P48281;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
GN Mus musculus (Mouse).
OS

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95137405; PubMed=7835717;
RA Kamel Y., Kawada T., Fukuwatari T., Ono T., Kato S., Sugimoto E.,
RT "Cloning and sequencing of the gene encoding the mouse vitamin D
RT receptor."
RL Gene 152:281-282(1995).
CC -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
CC THE EXPRESSION OF HORMONE SENSITIVE GENES.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NRI SUBFAMILY.

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CC or send an email to license@isb-sib.ch).

EMBL: D31969; BAA06737.1; -
DR HSR: P03372; 1HCO.
DR MGD: MGI:103076; VDR.
DR INTERPRO: IPR000324; -
DR INTERPRO: IPR000536; -
DR INTERPRO: IPR001628; -
DR PFAM: PF00104; hormone_rec; 1.
DR PFAM: PF00105; zf-C4; 1.
DR PRINTS: PR00047; STEROIDFINGER.
DR PRINTS: PR00350; VITAMINDR.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
DR RECEPTOR: Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Phosphorylation.
FT DNA_BIND 24 89 C4-TYPE ZINC FINGERS (TWO).
FT ZN_FING 24 44 C4-TYPE.
FT ZN_FING 60 44 C4-TYPE.
FT DOMAIN 90 186 HINGE.
FT DOMAIN 187 422 LIGAND-BINDING.
SQ SEQUENCE 422 AA; 47851 MW; 4704CC8172445732 CRC64;

Query Match 34.6%; Score 792.5; DB 1; Length 422;
Best Local Similarity 41.8%; Pred. No. 2.2e-56;
Matches 174; Conservative 74; Mismatches 127; Indels 41; Gaps 11;

38 POICRVCGDKATGYHFNWATCEGCKGFFRRAMRNALRCFFPKGACITRTKTRCOAC 97
DB 21 PRIGCVGDKATGYHFNWATCEGCKGFFRRAMRNALRCFFPKGACITRTKTRCOAC 97
QY 98 RLKRCESGKMKEMIMSDAVERALIKRKSEKSTGTOPLGVOGLTEORMMIRELMDA 157
DB 80 RLKRCVDMGKKEFLITDEVOARKREIMKREELALDLSRPK-LSEEQHIIAIIILDA 138
QY 158 QMKEFDTTFSHKKNFLP-GVLSSGCELP-----ESLQAPSR-BAKWS 200
DB 139 HKHTYPTIADPRFRPRVADSGSYSPRPLTSSGSSSSSSSLTYSIDMMEPASFS 198
QY 201 QVRKDCISLKLQKGEDESVNWKRPADSGKREIFSLPHVADSTYFKGIIIPAVYISFRD 260
DB 199 TM--DL-----NEGS-----DDPSVTLDLSPLSMLPHLADVSYSIOKVIQGFAMK 242
QY 261 ISYFRDLPTEDQISLKGAFELCOLRENTVFNNAETGTEGRLSYCLEDT---AGGFQO 317
DB 243 IPEFRDLTSDQIVLKSSAIEVIMKSNOSFTMDMSWDCSGSDYKYDVTVDYKAGHTELEPL 302
QY 318 LKFMKLKQLOLHEEYVLMQALISLSPRPGVQLQHRVVDQLOEOPALTKSYTECNRPQ 377
DB 303 ELLEPLIKFOYGLKLLHBEHVLMAICIVSPDRGVODAKLVEAIDRLSNTLQTYRCRRHP 362

QY 378 ECNRQPARHFLFKIMAMTELRSINAGHTQ--RLLRQIDHPF-APPLMQLF 430
 DB 363 RCHNPPGSHQLYAKKIOKLADRLSLNESHKQYRSLSPQENSMKLPVLVYFVG 418

RESULT 9
 VDR_BOVIN STANDARD; PRT; 424 AA.

ID VDR_BOVIN STANDARD; PRT; 424 AA.
 AC 028037;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-VUL-1999 (Rel. 38, Last annotation update)
 DE VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
 GN VDR OR NR1L1.
 OS Bos taurus; (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97034797; PubMed-8880453;
 RA Nelborge H.L., Bosworth B.T., Reinhardt T.A.;
 RT "Nucleotide sequence of the bovine vitamin D3 receptor."
 RL J. Dairy Sci. 79:1313-1315(1996).
 CC -1- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
 THE EXPRESSION OF HORMONE SENSITIVE GENES.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
 CC -1- NRI SUBFAMILY.
 CC -----
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 CC -----

DR EMBL; U50200; AAB01543.1;
 DR HSSP; P03372; IHCO.
 DR INTERPRO: IPR000324;
 DR INTERPRO: IPR000536;
 DR INTERPRO: IPR001628;
 DR PFAM; PF00104; hormone_rec; 1.
 DR PFAM; PF00105; zf-C4; 1.
 DR PRINTS; PRO0047; STROIDFINGER.
 DR PRINTS; PRO0350; VITAMINDR.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 KM Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 FT ZINC-FINGER; Phosphorylation. CA-TYPE ZINC FINGERS (TWO).
 FT DNA_BIND 21 86
 FT ZN_FING 21 86
 FT ZN_FING 57 81 CA-TYPE.
 FT ZN_FING 87 188 CA-TYPE.
 FT DOMAIN 189 424 HINGE.
 FT DOMAIN 189 424 LIGAND-BINDING.
 SQ SEQUENCE 424 AA; 47957 MW; E9E24926CE38CB7D CRC64;

Query Match 34.5%; Score 789; DB 1; Length 424;
 Best Local Similarity 42.2%; Pred. No. 4,1e-56;
 Matches 174; Conservative 67; Mismatches 143; Indels 28; Gaps 9;

QY 38 POICRVCGRATGYHFNVMTCGCGFFRRARNRALRCPPKAGCETTRKTRQCAQC 97
 DB 18 PRICVCGDRATGFHFNAMTCGCGFFRRARNRALRCPPKAGCETTRKTRQCAQC 76
 QY 98 RLKRCLESGKKKIMSDAVERBALIKKKKSERTGTPGLSVQGLTEPQKMKIRLMDA 157
 DB 77 RLKRCVIGMKKEFILDEVOQRKREMIKKEEALKQSLRPK-LSEQORIALIILDA 135

QY 158 QMKTFDTFSHFKNFLRPLGVLSG----CELPESLQAPSEEAQKNSQVRKDC----- 207
 DB 136 HNKTYDEPTVEQCFRPPVAVNDGCGSPSPSRNHTPS--FSGDSSSCSDHCITSSDM 193
 QY 208 ---SLKYSLALRGDGSVMYKPPADSGCKEIFSLPHMADMTYMKGLIISFAKXISYF 264
 DB 194 MDSSFSNLSLSEEDSD-----DPSTVLELSQJSMPLHDLVYSIQKYGAKMIPGF 248
 QY 265 RDLPIEDQISLKGAFELCOLRFNTVFNAETGWECCGRLSY---CLIEDYAGFOQLLE 321
 DB 249 RDLTSEQOYLTKSSALEVIMLRNENESTYMDMSKTCGNDYKRYSDYKASHLEIE 308
 QY 322 PMLFHYMLKQLHHEEYVLMQALISLSPDRGVQLHRYVDQLQEQFALTKSYIECNR 381
 DB 309 PLIKFVGKRLNHEEHVLMALICVSPDRGVQDALIEADRLSTLQTYINCRH 368
 QY 382 POPARHFLFKIMAMTELRSINAGHTQ--RLLRQIDHPF-APPLMQLF 430
 DB 369 PPSHLLYAKKIOKLADRLSLNESHKQYRSLSPQENSMKLPVLVYFVG 420

RESULT 10
 VDR_HUMAN STANDARD; PRT; 427 AA.

ID VDR_HUMAN STANDARD; PRT; 427 AA.
 AC P11473;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).
 GN VDR OR NR1L1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Plimates; Catarrhini; Homnidae; Homo.

[1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88217887; PubMed-2835767;
 RA Baker A.R., McDonald D.P., Hughes M., Crisp T.M., Mangelsdorf D.J.,
 RA Hausler M.R., Pike J.W., Shine J., O'Malley B.W.;
 RT "Cloning and expression of full-length cDNA encoding human vitamin D
 RT receptor."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:3294-3298(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92379083; PubMed-1324736;
 RA Goto H., Chen K.S., Prael J.M., Deluca H.F.;
 RT "A single receptor identical with that from intestine/747 cells
 RT mediates the action of 1,25-dihydroxyvitamin D-3 in HL-60 cells."
 RL Biochim. Biophys. Acta 1132:103-108(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97355582; PubMed-9212063;
 RA Miyamoto K., Kesterson R.A., Yamamoto H., Takekuni Y., Nishiwaki E.,
 RA Tatematsu S., Inoue Y., Morita K., Takeda E., Pike J.W.;
 RT "Structural organization of the human vitamin D receptor chromosome
 RT gene and its promoter."
 RL Mol. Endocrinol. 11:1165-1179(1997).
 RN [5]
 RP SEQUENCE OF 24-90 FROM N.A.
 RX TISSUE-PERIPHERAL BLOOD; PubMed-1850412;
 RX MEDLINE-91210272; PubMed-1850412;
 RA Yu X.-P., Mochizuki H., Hustwyler F.G., Manolagas S.C.;
 RT "Vitamin D receptor expression in human lymphocytes. Signal
 RT requirements and characterization by western blots and DNA
 RT sequencing."
 RL J. Biol. Chem. 266:7588-7595(1991).
 RN [6]
 RP VARIANTS ASP-33; AND GUN-73.
 RX MEDLINE-89072761; PubMed-2849209;


```

RESULT 13
NR13 MOUSE
ID NR13 MOUSE STANDARD: PRT: 358 AA.
AC 035627; 035628;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ORPHAN NUCLEAR RECEPTOR NR113 (CONSTITUTIVE ANDROSTANE RECEPTOR)
DE (CAR).
DE NR113 OR CAR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=97442417; PubMed=9295294;
RA Choi H.-S., Chung M., Zzameil I., Simha D., Lee Y.-K., Seol W.,
RA Moore D.D.;
RT "Differential transactivation by two isoforms of the orphan nuclear
RT hormone receptor CAR.";
RL J. Biol. Chem. 272:23565-23571(1997).
CC -1- FUNCTION: BINDS AND TRANSACTIVATES THE RETINOIC ACID RESPONSE
CC ELEMENTS THAT CONTROL EXPRESSION OF THE RETINOIC ACID RECEPTOR
CC BETA 2 AND ALCOHOL DEHYDROGENASE 3 GENS.
CC -1- SUBUNIT: HETERODIMER OF NR113 AND RXR.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAR1 (SHOWN HERE) AND CAR2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING. CAR2 DOES NOT SEEM TO ACT AS
CC A TRANSACTIVATOR.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR1 SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF009327; AAC53349.1; -
CC EMBL; AF009328; AAC53350.1; -
CC GDB; MGI:1346307; NR113.
CC INTERPRO; IPR000324; -
CC INTERPRO; IPR000356; -
CC INTERPRO; IPR001628; -
CC INTERPRO; IPR001723; -
CC INTERPRO; IPR001728; -
CC PFM; PFM0104; hormone_rec; 1.
CC PFM; PFM0105; zf-C4; 1.
CC PRINTS; PRO0047; STEROIDFINGER.
CC PRINTS; PRO0350; VITAMINR.
CC PRINTS; PRO0398; STROHORMONR.
CC PRINTS; PRO0546; THYROIDHORMR.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Activator; Alternative splicing.
CC DNA_BIND; 21; 86 C4-TYPE ZINC FINGERS (TWO).
CC FT DN_BIND 21 86 C4-TYPE.
CC FT ZN_FING 21 41 C4-TYPE.
CC FT ZN_FING 57 81 C4-TYPE.
CC FT VASPLIC 281 286 DRPVT -> GFCMQS (IN ISOFORM CAR2).
CC FT VASPLIC 287 358 MISSING (IN ISOFORM CAR2).
CC SEQUENCE 358 AA; 40894 MW; 4F07730FF78CABDC CRC64;

Query Match 31.7%; Score 725; DB 1; Length 358;
Best Local Similarity 39.3%; Pred. No. 4,6e-51;
Matches 157; Conservative 64; Mismatches 124; Indels 54; Gaps 6;
31 ADEYVSGPQICRCGCGKATGTHFNMTGCGCKGFFRRAMRNALRCFPFKGACETTRKT 90

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Db 11 ASEEYGRNVCYGDRTATGTHFHALTCCEGCKFFRTVSKTIGPICPF-AGRCVSKAQ 69
QY 91 RROCAACLRKCEGSKMKKIMSDEAVEERRALKRKSEKRGCTGPTGVGITEQRMA 150
Db 70 RRRPACACLOGLAVGRKDKITLSEALAKRRAQOVRKXSLD-----LNDQKEL 123
QY 151 IREIMADOMKTEPTDTSFHKFRLPGVLSGCELPESLAFSHEAAKMSQVAKDLSLK 210
Db 124 VOILGATHRHVGPLDQFVQFKPPAVL----- 151
QY 211 VSILREDSVWYKRPAPSGGKEIFSLPAPADSTYKFGIISFANVISYFDLPLE 270
Db 152 -----FMHRRPQPRG--PVLPLTHPADINTFWOQIIFTKDLPLFSLTWE 198
QY 271 DOISLNGAAFEICQLRFVFNATGTCWEGRLSYCLEDTA-GGFQOLLEPMLKPHM 329
Db 199 DOISLNGAAVEILHISLNTFTCLQDENPFCGLCKMEDAVHAGFOYEFELSLHFKN 258
QY 330 LKKQLHEEYVLMQATISLSPDRPGVLRHVVDQLOEOPATLTKSYIECNRPAPHRL 389
Db 259 LKGLHDEPYVLMATLSPDRPGVLRHVVDQLOEOPATLTKSYIECNRPAPHRL 318
QY 390 FLKIMAVLTELRSINQHQRLLRIODIHPRFAPLMOEL 428
Db 319 YAKIMGLADLNKSNINAYSTELQRLSELSAM-TPLLGEI 356

RESULT 14
NRH3_MOUSE STANDARD: PRT: 445 AA.
AC 0920Y9:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE OXYSTEROLS RECEPTOR LXR-ALPHA (LAYER X RECEPTOR ALPHA) (NUCLEAR ORPHAN RECEPTOR LXR-ALPHA).
GN NRH3 OR LXR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RA Chen Y.E., Horluchi M., Dzau V.J.
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ORPHAN RECEPTOR. INTERACTION OF LXR ALPHA WITH RXR SHIFTS RXR FROM ITS ROLE AS A SILENT DNA-BINDING PARTNER TO AN ACTIVE LIGAND-BINDING SUBUNIT IN MEDIATING RETINOID RESPONSES THROUGH TARGET GENES DEFINED BY LXRS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR1 SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF085745; AAD16050.1;
CC HSSP: P20393; 1A6Y.
CC INTERPRO: IPR000536;
CC INTERPRO: IPR001628;
CC PFM: PF00104; hormone_rec; 1.
CC PFM: PF00105; zf-C4; 1.
CC PRINTS: PR00047; STROIDFINGER.
CC PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger.
FT DN_BIND 96 161 C4-TYPE ZINC FINGERS (TWO).
FT ZN_FING 96 116 C4-TYPE.

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FT ZN_FING 132 156 C4-TYPE.
SQ SEQUENCE 445 AA: 50417 MW: 1A426DF38D935731 CRC64;

Query Match 21.8% Score 498.5; DB 1; Length 445;
Best Local Similarity 30.18; Pred.No. 9,2e-33;
Matches 129; Conservative 85; Mismatches 143; Indels 71; Gaps 13;

QY 18 EDTEVSGKISVNADEVGPOICRYCGDKATGYHFNWATCGCKGFFRRAMKRNARLC 77
Db 73 EPELPRQKRRKPPAKMGLNGLSYCGDKAGFHYNTLSGCGCGFFRRYVIGARLYC 132
QY 78 PFRKGCETIRKRRQCAQLRKCEGSKMKKIMSDEAVEERRALKRKSE----- 131
Db 133 -HSGGCPMEITYRRKQCCRLKCRQAGMRECVLSEQIILRK--LKQEEQQAQATS 189
QY 132 ---RTGTPGVGGLTEEDRRMIRELMDOMKTEPTDTSFHKFRLPGVLSGCELPESL 188
Db 190 VSPRVSSPCVLPQSLPBDLGMIEKLVAAQDCNRST----- 228
QY 189 QAPSRBAARWQVRKDCSLKVSQLRGSDSVWYKRPAPSGGKEIFSLPAPADST 248
Db 229 ---DRLRVTFW-PIAPD-----PQSRBAARQORA---HFTELAI 260
QY 249 YMKGIISPAKIVSYFRDLPIDQISILKGAAFELCOLRFNTVN--AETGTEGRLSY 306
Db 261 VSQVEIVDRKQPLQGLQSLREDQIALKTSATIEVMTLETSTRYRNPSSSITF-LKDFSY 319
QY 307 CLEDTA-GGFQOLLEPMLKPHMFKRLQLHEEYVLMQATISLSPDRPGVLRHVVDOL 365
Db 320 NREDFAKAGLOVEFINPIEFESRANNEQLDNDAPALLAISTISADPNVODQOVERL 379
QY 366 QDQFATLTKSYIECNRPAPHRLFLKIMAVLTELRSINQHQRLLRIODIHPRAP 423
Db 380 QHTYVLAALVYSINHPDP--LKEPRMIAVLVSLRTISVSHQVVALRLQD--KRLPP 435
QY 424 LMQELFGI 431
Db 436 LLSLEIMDV 443

RESULT 15
NRH2_HUMAN STANDARD: PRT: 461 AA.
AC P55055:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE OXYSTEROLS RECEPTOR LXR-BETA (LAYER X RECEPTOR BETA) (NUCLEAR ORPHAN RECEPTOR LXR-BETA) (UBIQUITOUSLY-EXPRESSED NUCLEAR RECEPTOR).
DE RECEPTOR NER.
GN NRH2 OR LXR2 OR UXR OR NER.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RA MEDLINE-95011628; Pubmed-7926814;
RX Shinar D.M., Endo N., Rutledge S.J., Vogel R., Rodan G.A., Schmidt A.;
RT "NER, a new member of the gene family encoding the human steroid hormone nuclear receptor."
RL Gene 147:273-276(1994).
CC -1- FUNCTION: ORPHAN RECEPTOR. BINDS PREFERENTIALLY TO DOUBLE-STRANDED OLIGONUCLEOTIDE DIRECT REPEATS HAVING THE CONSENSUS HALF-SITE SEQUENCE 5'-AGGTCA-3' AND 4-NT SPACING (DR-4).
CC -1- SUBUNIT: FORMS A HETERODIMER WITH RXR.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR1 SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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Description
thyroid hormone receptor
vitamin d receptor
vitamin b ₁₂ -dimethylcobalamin receptor
vitamin d receptor
vitamin d receptor
vitamin d receptor
vitamin d receptor
nuclear hormone receptor
steroid hormone receptor
steroid hormone receptor
nuclear orphan receptor
retinoid x receptor
orphan nuclear receptor
farnesoid x-receptor
retinoid x receptor
thyroid hormone receptor
beta-thyroid hormone receptor
gene c-ret/a, beta 1
thyroid hormone receptor
thyroid hormone receptor
thyroid hormone receptor
thyroid hormone receptor
thyroid hormone receptor
thyroid hormone receptor
thyroid hormone receptor
retinoic acid receptor
retinoic acid receptor
retinoic acid receptor
cdysone receptor

020 41DSVNEFFSFJNKKLLIPLKIMECLTELRIVNDIHSKQLLEIMDIPDPTPLMREVEFG 383

RESULT 2

vitamin D receptor subtype a - Paratichthys olivaceus

C:Species: Paratichthys olivaceus

C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 18-Aug-2000

C:Accession: J07229

R:Suzuki, T.; Suzuki, N.; Sivasubramanian, A.S.; Kurokawa, T.

Biochem. Biophys. Res. Commun. 270, 40-45, 2000

A:Title: Identification of cDNAs encoding two subtypes of vitamin D receptor in flounder

A:Reference number: J07229

A:Accession: J07229

A:Molecule type: mRNA

A:Residues: 1-420 <SUZ>

A:Cross-references: DBJ:AB037673

A:Experimental source: Intestine

C:Comment: This receptor is an important factor in calcium homeostasis and bone formation

C:Keywords: bone; calcium transport; DNA binding; hormone receptor; intestine; vitamin D

Query Match 35.7%; Score 817; DB 2; Length 420;

Best Local Similarity 43.1%; Pred. No. 3e-56; Mismatches 144; Indels 22; Gaps 12;

Matches 179; Conservative 70;

29 VNAD-EEGPGQICRGVGRATGTFHNVMTCEGKFFRRAMRNALRCPPKAGCEIT 87

11 VGPEFRNAPRIGCGVGRATGTFHNVMTCEGKFFRRAMRNALRCPPKAGCEIT 69

88 KTRRQOCARLRCESGKKEKIMDEVEERALLIRKKSERCTGTOPLGVOGLTEQ 147

70 KDNRRHOCARLRCESGKKEKIMDEVEERALLIRKKSERCTGTOPLGVOGLTEQ 128

148 RMNRELDQOMKTEFTTFSHKFRRLP---GVLSSGCELPESIQAPSRREAAKWSQVR 204

129 ARMTSSIVEAHKHTYDSYDFSRFPVREGPTRSASAAASHLSDSNDSFNNISPE 188

205 DLCSLKV---SLDRGDSGVWNYKPPADSGKEIFSLPLHADMSTYFKGIISPAKV 261

189 SV-DTKNFSLLAMYQDA---SSPDSSEENTKLSMLPLADLVYSIOKVIYGFAMKI 243

262 SYFDLPLEDIOISLKGAPFICOLRRNTYVNAATGWECS-RLSTCLSD-PAAGGQOL 318

244 PGFDLDAEDDIALKSSALEIIMKRSNQSFLSDMSGCGPDKYCINDVTKAGTLE 303

319 LLEPLMKFHYMLKRIQLHEEYVLMQALISLSPDPGVLQHRVVDQLQEQFATLTKSYIE 378

304 LLEPLVDFQVGLKRLNHEEHVLMQALISLSPDPGVLQHRVVDQLQEQFATLTKSYIE 363

379 CNRPQAHRELFLEKIMAMLELRSINMOHTO--RLRIQDIHFP-APPLMOELFG 430

364 IN--HPGRLLYAKMIQIADLRSLNHEHSHKQYRSLSPQESHSMQPLVLEVFG 416

RESULT 3

vitamin D receptor isoform A - Japanese quail

C:Species: Coturnix coturnix japonica (Japanese quail)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999

C:Accession: U05451

R:Elarousli, M.A.; Prah, J.M.; Deluca, H.F.

Proc. Natl. Acad. Sci. U.S.A. 91, 11586-11600, 1994

A:Title: The avian vitamin D receptors; primary structures and their origins.

A:Reference number: U05451; MUID:95062315

A:Accession: U05451

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-448 <ELAR>

A:Cross-references: EMBL:U12641; NID:9595500; PIDD:AA56725.1; PID:9595501

C:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: zinc finger

F:42-362/Domain: erba transforming protein homology <ERBA>

Query Match 35.6%; Score 815.5; DB 2; Length 448;

Best Local Similarity 40.9%; Pred. No. 4.2e-56;

Matches 179; Conservative 72; Mismatches 154; Indels 33; Gaps 10;

17 CEDDE---SVGRKPSVNADE-EEGPGQICRGVGRATGTFHNVMTCEGKFFRRAMRN 72

16 CESELOSSDETFEAVGTPEFDRNVPRICGVDRAIGFHNATCEGKFFRRAMRN 75

73 ARLCPFRKAGCEITRTKTRCOACRLKLESGKKEKIMDEVEERALLIRKKSER 132

76 AMFCPE-SDCKKITKDNRRHOCARLRCVDMKKEFILTDEYQKREKIMKREED 134

133 TGTPLQVQGTTEQGRKIMRIMQAKTDTTSHKFRRLP-----GVL 178

135 ALKESLKRK-SEBQOKVITNLEAHKHTYDTSNKRPPRKSFSSTATHSSVY 193

179 SSGCELPSLQAPSRREAAKWSQVRKDLCSLKVSLDRGDSGVWNYKPPADSGKEIFS 238

194 SODPSSEDSNDVFGSDAFAPPEMEPQMSNDLSEDSSESPMNTELP-----LP 246

239 LLEPMADMSTYFKGIISPAKVSYFDLPLEDIOISLKGAPFICOLRRNTYVNAATGT 298

247 MLPPLADLVYSIOKVIYGFAMKIPGFDLDAEDDIALKSSALEIIMKRSNQSFLSDMS 306

299 WECGR-LSYCLSD-PAAGGQOLLEPLMKFHYMLKRIQLHEEYVLMQALISLSPDPG 355

307 WTCGSNDRKRYVSDTQGHSMDLLEPLVDFQVGLKRLNHEEHVLMQALISLSPDPG 366

356 VLOHVRVDQLQEQFATLTKSYIECNRPQAHRELFLEKIMAMLELRSINMOHTO--RLR 413

367 VQDTLVESIDRLSDIQTQYIRCHNRRPGRSLLYAKMIQIADLRSLNHEHSHKQYRCL 426

414 IODIHPF-APPLMOELFG 430

427 FQPEHSMQPLVLEVFG 444

RESULT 4

1,25-dihydroxyvitamin D-3 receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Sep-1999

C:Accession: A31761; A31367

R:Burnester, J.K.; Wiese, R.J.; Maeda, N.; Deluca, H.F.

Proc. Natl. Acad. Sci. U.S.A. 85, 9499-9502, 1988

A:Title: Structure and regulation of the rat 1,25-dihydroxyvitamin D-3 receptor.

A:Reference number: A31761; MUID:89071726

A:Accession: A31761

A:Molecule type: mRNA

A:Residues: 1-423 <BUR>

A:Cross-references: GB:J04147; GB:J03630; NID:9203956; PIDD:AAA41089.1; PID:9203957

R:Burnester, J.K.; Maeda, N.; Deluca, H.F.

Proc. Natl. Acad. Sci. U.S.A. 85, 1005-1009, 1988

A:Title: Isolation and expression of rat 1,25-dihydroxyvitamin D-3 receptor cDNA.

A:Reference number: A31367; MUID:88124963

A:Accession: A31367

A:Molecule type: mRNA

A:Residues: 1-423 <SUZ>

C:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: DNA binding; transcription regulation; zinc finger

F:22-337/Domain: erba transforming protein homology <ERBA>

F:24-44/Region: zinc finger

F:60-84/Region: zinc finger

Query Match 35.0%; Score 801; DB 2; Length 423;

Best Local Similarity 42.0%; Pred. No. 5.3e-55;

Matches 172; Conservative 75; Mismatches 135; Indels 28; Gaps 9;

38 PQICRGVGRATGTFHNVMTCEGKFFRRAMRNALRCPPKAGCEITRTTRGQAC 97

[illegible]

RESULT 5

PC4019

Vitamin D receptor - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 26-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Sep-1999

C:Accession: PC4019

R:Kamei, Y.; Kawada, T.; Fukuwatari, T.; Ono, T.; Kato, S.; Sugimoto, E.

Gene 152, 281-282, 1995

A:Title: Cloning and sequencing of the gene encoding the mouse vitamin D receptor.

A:Reference number: PC4019; MUID:95137405

A:Accession: PC4019

A:Molecule type: mRNA

A:Residues: 1-422 <KAA>

A:Cross-references: DDBJ:D31969; NID:669618; PIDD:BAA06737.1; PID:41007311; PID:6699613

C:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: DNA binding; zinc finger

F:22-336/Domain: erba transforming protein homology <ERBA>

F:24-89/Domain: DNA binding #status predicted <BIN>

F:191-422/Region: Vitamin D binding #status predicted

```

Query March Similarity      34.6%: Score 792.5; DB 2; Length 422;
Best Local Similarity      41.8%: Pred. No.2.4e-54;
Matches 174; Conservative   74; Mismatches 127; Indels 41; Gaps 11;

QY    38 POICVCGDMMATGYHFNWMTCEGCKGFRRFRAKRNARLRCPFRKAGACETTRTKRQCAC 97
       ||| ||||| ||||| ||||| ||||| ||||| ||| ||| ||| |||
Db    21 PRIGCVGGDRATGFIHFNAATCEGCKGFFRRSRKRALTCRP--NDCKITKDNRHCAC 79
       ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY    98 RLRLCLESGRMKREIMSDAEVEERRALIRKKSEPTGTOPLGVOGLTEORAMIRELDA 157
       ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    80 RLKRCVDIGMKNKEFLTDEYQRKREMIKRKEELALDSLRK-LSEQQIILILLDA 138
       ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY    158 QMKRTDTTFSHPKRNRLP--GVLSGCCLP-----ESLAQPSRE--EAAWTS 200
       ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db    139 HHKTDPDYAEFRDFPRPIRADVSTGSYSPPRTLSPSGDSSNSDLTYPLSLDMPEAFS 198
       ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

QY    201 OVRKDLGLKLVSLDARGDGSVWNKKPPADSGRKIFSLPMPADMNSTYMFGIIISPAKV 260
       : || : || : || : || : || : || : || : || : || : || : || : ||
Db    199 TM--DL-----NEGGS---DDPSVTLLDSLPLEMLPLDALVSYSLOKVIGFAKM 242
       : || : || : || : || : || : || : || : || : || : || : || : ||

QY    261 ISYFDLPLEDOQLSKAFAELCOLRENTVFNAETGWEGCRLSYCLEDT---AGGQQ 317
       ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    243 IPGFDLSDDOIVLLKSASAIETYMLRSNQSFYMDMSNDGCSODYKKYDIDVSAQHFL 302

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[illegible]

RESULT 6
JC7230
Vitamin D receptor subtype b - *Paralichthys olivaceus*
C:Species: *Paralichthys olivaceus*
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 18-Aug-2000
C:Accession: JC7230
R:Suzuki, T.; Suzuki, N.; Srivastava, A.S.; Kurokawa, T.
Biochem. Biophys. Res. Commun. 270, 40-45, 2000
A:Title: Identification of cDNAs encoding two subtypes of vitamin D receptor in flounder
A:Reference number: JC7229
A:Accession: JC7230
A:Molecule type: mRNA
A:Residues: 1-425 <SDSZ>
A:Cross-references: DDBJ:AB037674
A:Experimental source: Intestine
C:Comment: This receptor is an important factor in calcium homeostasis and bone formation
C:Genetics:
A:Gene: vdr-b
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: bone; calcium transport; DNA binding; intestine; vitamin D

Query Match	34.58;	Score 790.5;	DB 2;	Length 425;
Best Local Similarity	41.68;	Pred. No. 3.5e-54;		
Matches 179;	Conservative 78;	Mismatches 140;	Indels 33;	Gaps 13

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QY 22 SVPKPSPVNADE -EVGEPQICJCVGDKATGYNHNVMTCEGCKGFPFRMKNRLNCPFR 80
Db 4 TVSTSSLASBEPFRMNPRLICGVGDGATGTFHFNAMTCBEGCKGFPFRSMKRAKATTCPF- 62
QY 81 KGACEITRKTTRQOCACRLRKCLESNGKMKEMINSDEAVEERRALLIKRK-----SERT 133
Db 63 NGSCITRKNRRHCQACRLKCAVDIGKMRREFILDEVQKKDLQRRKDEQAOREARE 122
QY 134 GTQPLGVQGLIEBRRMIRRELMQAOMTFTPTTSHFNFLP---GYLSSGCLPESLCA 190
Db 123 ARRP-----RLDEQSOYIAMLVEAHNHTYDSDFCFRFPRAEGVYTIASARAALHS 178
QY 191 PSREAAKWSQVRDLCSLWKS-----LQLRGESQVYNYKPPADSGKEFTSLPHADM 246
Db 179 LSDASQSFSSPSMY-DITVNFNNLLMTMOEQS-----SPDSSEEGSSFSMLPHADL 223
QY 247 STYFKGILISAKVITSYFRDLPIEDQISLKGAAFELOCURENTVFNAETGTWECGR-L 304
Db 234 VSYIOGVIGAKKIPGFRRELTEDQJALLKSAIEVIMYLRMSQSFLEDMSSCGAPDF 293
QY 305 SYCED-TAGSFQOLLLEPLMKFHYMKIQLHBEEVYLMQAISLSPDPRGYLOHRYVD 363
Db 294 KYQISDVTAKGHITLEELPRLKFOVGAKTKNLTDEEBVYMLAICLSPDPGVOAHARIE 353
QY 364 QLOBOFAITLKSYIECNRPQPARHFLFKITAMALTELTSRINAQTO--RLRIYODIHFF- 420
Db 354 ALQORLSETLOAVYQLH--HPGGILYIAKKIQLADRLSLNEHSQYRSLSRPESHMQ 411
QY 421 ATPMLQFLFG 430
Db 412 LTPVLLEVSG 421

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RESULT 7
A28200
Vitamin D receptor - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 20-Sep-1990
```


Db 124 HMGMEFOVQFRPAHLFIHQ-PIETLAP----- 153
 Qy 221 SVMNKRPAADSGGKEISLPHMADSTYFVKGLISPAKVISYFRDLPTEDQISLLKGA 280
 Db 154 -----VPLTHRADINTFVNLVIRKFDLPVFRSLPTEDQISLLKGA 198
 Qy 281 FELCOLNFNTVFNATGTCGRLSYCLEDTAG-GFOQLLEPMLKFKHMLKRLQLEEE 339
 Db 199 VEICHIYLVNTFCLQTNFLCGLPLRTIEDGAVGFOVELLELFFHGTIRLQLQEP 258
 Qy 340 YVLMQALSLSPRPVGLQHRVVDQLOEOPATLKSYIECNRPQAPHRFLKIMAMTE 399
 Db 259 YVLAALALSPRPVGLQHRVVDQLOEOPATLKSYIECNRPQAPHRFLKIMAMTE 318
 Qy 400 LRSINAOHFORLRIODIHPFATPLMOEL 428
 Db 319 LRSINAEVGYOIHGIGLSAM-NPLIQEI 346

RESULT 10

JC4014
 steroid hormone-nuclear receptor NER - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Sep-1999
 C:Accession: JC4014
 R:Shinar, D.M.; Endo, N.; Rutledge, S.J.; Vogel, R.; Rodan, G.A.; Schmidt, A.
 Gene 147, 273-276, 1994
 A:Title: NER, a new member of the gene family encoding the human steroid hormone nuclear
 A:Reference number: JC4014; MUID:95011628
 A:Accession: JC4014
 A:Molecule type: mRNA
 A:Residues: 1-461 <SH>
 A:Cross-references: GB:U07132; MID:9641961; PIDN:AAA61783.1; PID:9641962
 A:Experimental source: osteosarcoma cells SAOS-2/B10
 C:Genetics:
 A:Gene: GDB:UNR
 A:Cross-references: GDB:389570; OMIM:600380
 A:Map position: 19q13.3-19q13.3
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: steroid hormone receptor
 F:85-381/Domain: erba transforming protein homology <ERBA>
 F:87-154/Domain: DNA binding #status predicted <BIN>

Query Match 21.7%; Score 498; DB 2; Length 461;
 Best Local Similarity 29.0%; Pred. No. 2.6e-31;

Matches 126; Conservative 86; Mismatches 125; Indels 98; Gaps 14;

Qy 37 GPQIRVCGDKATGYHFNVTCEGCKGFFRRAMRNALRCRFR-KGACETTRTRQCO 95
 Db 83 GHELCRVGDKASGFHYNLVSCGCKGFFRRSVVGARFACRGCGTCQMDAFWRRCQ 142
 Qy 96 ACRLKCLESGKMKMSIDEAVERALLIRKKSERTGT-PIGVG----- 142
 Db 143 OCLRAKCEAGRCRCVSEEDIRKK--IRKQOQESOSOSVGVGSSSSASGPGA 200
 Qy 143 -----LTEORMIRELMDAQMTFTDTSFKNFRPLPVLSGCE 183
 Db 201 SPGSEAGSOGSGEGVQLTNAQELMIQVLAQLOCNKRSF----- 244
 Qy 184 LPESLOASREBAKWSVRKDCSLAKVSLQKRGEDGSVMYKRPADSGGKEIFSLPHM 243
 Db 245 -----DQPVTPW-----LGND-----POSRDARQORFA--HF 271
 Qy 244 ADMSTYFKGIISPAKVISYFRDLPTEDQISLLKGAELCOLNFNTVFNATGTCWEC-- 301
 Db 272 TELAIISVQELVDPAKQVPGFLQLOREDQIMLKASTIEMLTARRYNHET--ECIT 328
 Qy 302 --GRISTYLED-TAGGFOQLLEPMLKFKHMLKRLQLEEEYVLMQALSLSPRPVGLQ 358
 Db 329 FLKDTYKSDPFHRAQLQVEFINDIFEFSSRAMRRLGLDDAEYALLAINIFSDRPAVQE 388

Qy 359 HRVVDQLOEOPATLKSYIECNRPQAPHRFLKIMAMTELRISINAOHFORL-LRIOD 416
 Db 389 PERVALDQFVEALSTRIKRPQDOLR-FPRMIMKLVSIRLTSVSHSEVAFALRIOD 446
 Qy 417 IHPFATPLMOELFGI 431
 Db 447 --KKRPLSLSEIMDV 459

RESULT 11

A56043
 steroid hormone receptor-like protein RLD-1 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 24-Sep-1999
 C:Accession: A56043
 R:Apfel, R.; Benbrook, D.; Lernhardt, E.; Ortiz, M.A.; Salbert, G.; Pfehl, M.
 Mol. Cell. Biol. 14, 7025-7035, 1994
 A:Title: A novel orphan receptor specific for a subset of thyroid hormone-responsive
 A:Reference number: A56043; MUID:95021230
 A:Accession: A56043
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-445 <APF>
 A:Cross-references: GB:U11685; MID:9555751; PIDN:AAA53633.1; PID:9555752
 A:Note: Authors translated the codon GAG for residue 73 as Ser
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: steroid hormone receptor; zinc finger
 F:94-365/Domain: erba transforming protein homology <ERBA>

Query Match 21.7%; Score 496.5; DB 2; Length 445;
 Best Local Similarity 30.1%; Pred. No. 3.3e-31;

Matches 129; Conservative 84; Mismatches 144; Indels 71; Gaps 13;

Qy 18 EDIESVGRKSVNADDEVGQPOICRVCGDKATGYHFNVTCEGCKGFFRRAMRNALRC 77
 Db 73 EPTELRPQKRRKGPAPKMLGNELCSVCGDKASAFHYNLVSCGCKGFFRRSVYKGRYIC 132
 Qy 78 PFRGACETIRKTRRQCOACRLKCLESGKMKMSIDEAVERALLIRKKSE----- 131
 Db 133 -HSGCHCPMTYMKRKQCECRKRCAGRCRCVSEEDIRKK--LRQEEQAOATS 189
 Qy 132 ---RTGTPGVGLTEEQRMIRELMDAQMTFTDTSFKNFRPLPVLSGCEPESL 188
 Db 190 VSPRVSSPPQVLPOLSPEDQIGMETKLVAAQOQCNRSFS----- 228
 Qy 189 QADSRBAKWSVRKDCSLAKVSLQKRGEDGSVMYKRPADSGGKEIFSLPHMADMT 248
 Db 229 ---DRLVTPW-PIADP-----POSREARQORFA--HTELAI 260
 Qy 249 YMKGIISPAKVISYFRDLPTEDQISLLKGAELCOLNFNTVFN--AETGWECCRLSY 306
 Db 261 VSVQELVDPAKQVPGFLQLOREDQIMLKASTIEMLTARRYNHET--ECIT 319
 Qy 307 CLEEDTA-GGFOQLLEPMLKFKHMLKRLQLEEEYVLMQALSLSPRPVGLQHRVVDL 365
 Db 320 NREDPAKAGIQVEFINDIFEFSSMNELOLNAERFLLAISIFSDRPNVDQLOVEFL 379
 Qy 366 QEOPATLKSYIECNRPQAPHRFLKIMAMTELRISINAOHFORL-LRIODIHPFATP 423
 Db 380 QHTYVETALHAYVSIHNP--DRLMFPRLMKLVSLRTISSVHSEGVFLRLDD--KKLP 435
 Qy 424 LMOELFGI 431
 Db 436 LLSSEIMDV 443

RESULT 12

138975
 nuclear orphan receptor LXR-alpha - human
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 20-Sep-1999
 C:Accession: I38975


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Db 74 GHELCVNCDDKASGFHYNYLSCGCGFRRSRVHGAGRYACRSGGTCQDAFERRCQ 133
OY 96 ACRLRCLSGMKRKMINSDEAVEERRLIRKKSERGTOLP----- 138
Db 134 LCLRLRCNKGMEQCVLSEEDIRKKIKQKQOOPPPPTPAGSSARPAASPTSEAS 193
OY 139 -----GVQGLTEQRMIRELMDAOKRTDTTFSHKFNRLPGVLSGCELPESLQA 190
Db 194 SGGSGEGEIO-LTAAQELMIQOLVAQLOCKRKSFS----- 229
OY 191 PSREAAKRSQYRKDCLSKVSLQRGEDGSWMNKKPAGSGGKEITSLPMDMSTYM 250
Db 230 -DQPKTTPP-----LGAD-----PQSRDARQORFA--HETELATIS 263
OY 251 FPGIISFAKVISYFRDLPEDDISILKGAFAELCOLRNTFYNAETGWEC---GLTSY 306
Db 264 VOEIVDFAKQVPGFLQGRDQIALTKASTIEIMLETKARNYNET--ECITFLKDETY 320
OY 307 CLED-TAGGFQOLLPEPLKFKHYMLKQLHEEYVLMQALSLFSPDPGVLQHRVVDL 365
Db 321 SKDDEHRRAGLOVEFNPTFEFSRAMRRLGLDAEYALLIAINIFSADRPVNOEPSREAL 380
OY 366 QEOFAITLTKSYECNRPOPARHFLFKIMAMLTLSINAOHTOL--LRIDIHPPATP 423
Db 381 QOPYEALLSTYRKIRKPODOLR--FPRLMKLVSLKTLSSVSHSQVAFRLQD--KKLP 436
OY 424 LMOELFGI 431
Db 437 LLSEITWY 444

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RESULT 15

A56918

farnesoid x-activated receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 24-Sep-1999

C:Accession: A56918

R:Forman, B.M.; Goode, E.; Chen, J.; Oro, A.E.; Bradley, D.J.; Perlmann, T.; Noonan, D.J.

Cell 81, 687-695, 1995

A:Title: Identification of a nuclear receptor that is activated by farnesol metabolites.

A:Reference number: A56918; MUID:95292336

A:Accession: A56918

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-469 <FOR>

A:Cross-references: GB:U18374; NID:9868031; PIDN:AC52205.1; PID:9868032

C:Superfamily: unassigned erba-related proteins; erba transforming protein homology

C:Keywords: DNA binding; nucleins; zinc finger

F:122-390/Domain: erba transforming protein homology <ERBA>

Query Match

Best Local Similarity 19.9%; Score 456; DB 2; Length 469;

Matches 130; Conservative 78; Mismatches 146; Indels 100; Gaps 16;

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OY 5 PKESWNHADVFCEDETE---SVPKPSVNADE--EVGAPQICRYCGDKATGHEHNTWC 58
Db 88 PTES-----VYQGETVESEMPYTKPRMAASAGRIKGEIDELCYVCGDRASGYHNAITC 141
OY 59 ECGKGFERRAMRNARLKPFRKACETITRTROCCACRLKCLSGMKKEMIMSDAV 118
Db 142 ECGKGFRSRSTIKNAVYKCK-NGNCVMDMYRRKQDCRLKRCREMGMLAECLLTIEIC 200
OY 119 EERRALIRKKKSERTGTOLGVQ-----LTREQRMARELMDQMK 160
Db 201 KSKR-LRKRVKQHADQYVNESEGDHLQOVYSTKLCREKTELTVDDQTLIDYIMDSYK 259
OY 161 TDDTFSHKFNRLPGVLSGCELPESLQAPSREAAKMSQVRKDLCLKVSLLQRGEDG 220
Db 260 Q-----RMPQET-----NKILKE----- 273
OY 221 SVMNKKPPADSGKEIFSLPLPHMADMSTYMKGIISFAKVISYFRDLPEDDISILKGA 280

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Db 274 -----EFSAEENFLIL--TEMATSHVQILVEFTKRLPGQTIDHEDQIALKGA 321
OY 281 FELCOLRFTVYVNAETGWEGGRSLSYCLEDTAGGFQOLLPEPLKFKHYMLKQLHEEY 340
Db 322 VEMAFLRSEITPKKLPAGHADLLEERTKS--GISDEYITPMSEFYKSVGEIKMQOEY 379
OY 341 VLMQALISFSDRPGVLOHRVVDLOEQFAITLTKSYIECNRPQ-PAHREFLKIMAMLT 399
Db 380 ALLTAIVILSPDROKIKDREAVEKQLQEPDLVLOKCKLTIQEPNPH--FACLLGRTE 436
OY 400 LRSINAOHTORLL--RIODIHPPATP LMOELFGI 431
Db 437 LRTFNHHAEMLMMSRVND-HKF-TPLICEITWY 468

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Search completed: February 18, 2001, 14:33:07
 Job time: 5356 sec

